

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: April 28, 2005, 00:40:20 ; Search time 13971 Seconds
(without alignments) 7931.936 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVPRCVRTPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Xgapop	10.0	, Xgapext	0.5
Ygapop	10.0	, Ygapext	0.5
Fgapop	6.0	, Fgapext	7.0
Delop	6.0	, Delext	7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Command line parameters:

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool/US09611257/runat_26042005_150449_14893/app_query.fasta_1.2439
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257@cgn_1_1_8809@runat_26042005_150449_14893 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : GenEmbl : ★

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1: gb_ba:*
2: gb_hrg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	12024	100.0	7540	6	AX068898	Sequence
2	11980	99.6	6942	10	AF290212	Rattus no
3	11980	99.6	7542	10	RNCAA1G	AF027984 Rattus no
4	11829	98.3	7285	6	BD224079	BD224079 T-type ca

Percent Similarity: 100.00%		Conservative: 0	
Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 99.97%		Indels: 0	
DB: 6		Gaps: 0	
US-09-611-257A-24 (1-2287) x AX068898 (1-7540)			
QY	1	MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg	20
Db	385	ATGCTCCCCACCGGGTCCCCCGTTGGCTGAGGACACCTCTCTGAGGGGCTCCGCTCGC	444
QY	21	ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu	40
Db	445	CCCTCTTCGACCCCGGGGCCCGCTGGCCAGAGGATGGACGAGGAGGATGGAG	504
QY	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly	60
Db	505	CGGGCGCCGAGGAGTCGGGACAGCCCCCGTAGCTTCACGCAGCTCAACGACCTGTCCGGGG	564
QY	61	ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla	80
Db	565	CCGGGGCGGCAGGGGCCGGGTCCAGCGGAAAGGACCCGGGCGAGCGCGACTCCGAGGCG	624
QY	81	GluGlyLeuProTrpProAlaLeuAlaProValValPhePheTrpLeuSerGlnAspSer	100
Db	625	GAGGGGCTGCCGTACCCCGCGCTAGCCCCGGTGGTTTCTTCTACTTGAGCCAGGACAGC	684
QY	101	ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet	120
Db	685	CGCCCCGGGAGCTGGTGTCTCCGACCGGTCTGTAAACCCGTGGTTCGAGCGAGTCAGTATG	744
QY	121	LeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAla	140
Db	745	CTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCCGTGTGAGGACATTGCC	804
QY	141	CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePhe	160
Db	805	TGTGACTCCCAGCGCTGCCGATCCTGCAGGCCTTCGATGACTTTCATCTTTGCCCTTCTTT	864
QY	161	AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTrpLeu	180
Db	865	GCTGTGGAATGGTGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAGAAATGTTACCTG	924
QY	181	GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTrpSer	200
Db	925	GGAGACACTTGGAACCGGCTTGACTTTTTCATTGTTCATTGCAGGGATGCTGGAGTATTCG	984
QY	201	LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu	220
Db	985	CTGGACCTGCAGAACGTTCAGCTTCTCCGCACTCAGGACAGTCCGTGTGTCGACCGCTC	1044
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu	240
Db	1045	AGGGCCATTAAACCGGTGCCACAGATGCGCATTTCTCGTCACATTACTGTGGACACCTTG	1104
QY	241	ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal	260
Db	1105	CCTATGCTGGGCAACGTCTGCTGCTGTTTCTTCGTTCTTTTTCATCTTTTGGCATCTG	1164
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
Db	1165	GGCGTCCAGCTGTGGCAGGACTGCTTCGCAACCGGTGCTTCTCTCCCGAGAACTTCAGC	1224
QY	281	LeuProLeuSerValAspLeuGluProTrpTrpGlnThrGluAsnGluAspGluSerPro	300
Db	1225	CTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAAATGAGGACGAGAGCCCC	1284
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
Db	1285	TTCATCTGCTCTCAGCCTCGGAGAATGGCATGAGATCCTGCAGGAGTGTGCCACACTG	1344
QY	321	ArgGlyGluGlyGlyGlyGlyProProCysSerLeuAspTrpGluThrTrpAsnSerSer	340

Db	1345	CGTGGGAAGCGGTGTGTGGCCCAACCTTGCAGTCTGGACTATGAGACCTATAACAGTTCC	1404
QY	341	SerAsnThrThrCysValAsnTrpAsnGlnTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp	360
Db	1405	AGCAACACCACTGTGTCAACTGGAACCACTACTATACCAACTGTCTGCGGGCGAGCAC	1464
QY	361	AsnPropheLysGlyAlaIleAsnPheAspAsnIleGlyTrpAlaTrpIleAlaIlePhe	380
Db	1465	AACCCCTTCAAAGGCGCCATCAACTTTGACAACTTTGGCTATGCCTGGATCGCCATCTTC	1524
QY	381	GlnValIleThrLeuGluGlyTrpValAspIleMetTrpPheValMetAspAlaHisSer	400
Db	1525	CAGGTCAATCACACTGGAGGCTGGTGCACATCATGTACTTCTGTAATGGACGCTCACTCC	1584
QY	401	PheTrpAsnPheIleTrpPheIleLeuLeuIleValGlySerPhePheMetIleAsn	420
Db	1585	TTCTACAACTTCATCTACTTCAATTTCTTCATCATCTGGGCTCCTTCTTCATGATCAAC	1644
QY	421	LeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu	440
Db	1645	CTGTGCTGTGTGATTGCCACGCAGTTTCTCCGAGACCAACAGCGGGAGAGTCAGCTG	1704
QY	441	MetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlu	460
Db	1705	ATGCGGGAGCAGCGTGTACGATTCTGTCCAATGTAGCACCTTGGCAAGCTTCTCTGAG	1764
QY	461	ProGlySerCysTrpGluGluLeuLysTrpLeuValTrpIleLeuArgLysAlaAla	480
Db	1765	CCAGGCAGCTGCTATGAGGAGTACTCAAGTACCTGGTGATACATCCTCCGAAAAGCAGCC	1824
QY	481	ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPro	500
Db	1825	CGAAGGCTGGCCCCAGGTCTCTAGGGCTATAGCGGTGGGGTGGGCTGCTCAGCAGCCCA	1884
QY	501	ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg	520
Db	1885	GTGGCCCGTAGTGGGCGAGGAGCCCGAGCCCGAGTGGCAGTGCACCTGCACACCGTCT	1944
QY	521	LeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHis	540
Db	1945	CTGTCTGTCCACCACCTGGTCCACCACCATCACCCACCATCACCTACCCACTACCACTGGGT	2004
QY	541	AsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly	560
Db	2005	AATGGACGCTCAGAGTTCCCCGGGCGAGCCAGAGATCCAGGACAGGGATGCCAATGGG	2064
QY	561	SerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg	580
Db	2065	TCTCGCCGGCTCATGTATCCACCACCTCTACACCCACTCCCTCTGGGGGCCCCTCCGAGG	2124
QY	581	GlyAlaGluSerValHisSerPheTrpHisAlaAspCysHisLeuGluProValArgCys	600
Db	2125	GGTGGGAGTCTGTACACAGCTTCTACCATGTGACTGTGACTGCCACTTGGAGCCAGTCC	2184
QY	601	GlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys	620
Db	2185	CAGGCACCCCTCCAGATGCCCATCGGAGGCATCTGCTAGGACTGTGGGTAGTGGGAAG	2244
QY	621	ValTrpProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuVal	640
Db	2245	GTGTACCCCACTGTGCATACCAGCCCTCCACAGAGATACTGAAGGATAAAGCACTAGTG	2304
QY	641	GluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyPro	660
Db	2305	GAGGTGGCCCCCAGCCCTGGGCCCCCCCCCTCACAGCTTCAACATCCACCTGGGCC	2364
QY	661	PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys	680
Db	2365	TTGAGCTCCATGCACAAGCTCTCTGGAGACACAGAGTACGGGAGCTGCCATAGCTCCTGC	2424
QY	681	LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro	700
Db	2425	AAAATCTCCAGCCCTTGTCTCCAAGGCAGACAGTGGAGCCTTGGGGCGGACAGTTGTCCC	2484

QY 701 TyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSer 720
Db 2485 TACTGTGCCCGACAGGACGAGAGGACGAGTCCGCTGACCATGTCTATGCCTGACTCA 2544
QY 721 AspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro 740
Db 2545 GACAGCGAGGCTGTGTATGAGTTTCACACAGGACGCTCAGCACAGTGACCTCCGGGATCCC 2604
QY 741 HisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla 760
Db 2605 CACAGCCGGCGCACAGCGGAGCCTGGGCCCAGATGCAGAGCTAGTTCTGTGTGGCT 2664
QY 761 PheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArg 780
Db 2665 TTCTGGAGGCTGATCTGTGACACATTCGGGAAGATCGTAGATAGCAAAATACTTTGGCCGG 2724
QY 781 GlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGln 800
Db 2725 GGAATCATGATCGCCATCTGGTCAATACACTCAGCATGGGCATCGAGTACCACGACGAG 2784
QY 801 ProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAla 820
Db 2785 CCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACATCGTTTCACGAGCCTCTTCGCC 2844
QY 821 LeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyr 840
Db 2845 TTGGAGATGCTGTGAAACTGCTTGCTACGGTCCCTTTGGGTACATTAAAGAAATCCCTAC 2904
QY 841 AsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGly 860
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QY 861 GlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe 880
Db 2965 GGTGGCCTGTGGTGTCTCGGACCTTCGGCCTGATGCGGGTGTGTGAAGCTGTGGCTTC 3024
QY 881 LeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThr 900
Db 3025 CTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATGAAGACCATGGACAACGTGGCCACC 3084
QY 901 PheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPhe 920
Db 3085 TTCTGCATGCTCTCATGCTGTTTCATCTTCATCTTCAGCATCTGGGCATGCATCTCTT 3144
QY 921 GlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsp 940
Db 3145 GGTTGCAAGTTCCGATCTGAACGGGATGGGACACGTTGCCAGACCCGGAAGAAATTCGAC 3204
QY 941 SerLeuLeuTrpAlaIleValThrPheGlnIleLeuThrGlnGluAspTrpAsnLys 960
Db 3205 TCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATTCTGACTCAGGAAGACTGGAAATAA 3264
QY 961 ValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeu 980
Db 3265 GTCCCTCTACACGGCATGGCCTCCACATCGTCTTGGGCTGCTCTTTACTTCATCGCCCTC 3324
QY 981 MetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPhe 1000
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QY 1001 GlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal 1020
Db 3385 CAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTCGCCCATGTG 3444
QY 1021 AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
Db 3445 GATGGTATGGGACAGAAAGCGCTTGGCCCTGGTGGCTTGGGAGAACACCGCGAA 3504
QY 1041 LeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHis 1060
Db 3505 CTACGAAAGAGCCTTTTGGCACCCCTCATCATCCATACGGTGGGACACCAATGTCACAC 3564

QY 1061 ProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSer 1080
Db 3565 CCCAAGAGCTCCAGCACAGGTGTGGGGAAGCACTGGGCTCTGGCTCTCGACGTACCAGT 3624
QY 1081 SerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAla 1100
Db 3625 AGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAAATGTCCGCCAAGTGCC 3684
QY 1101 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSerSer 1120
Db 3685 CGCAGCTCCCGCACAGTCCCTGGAGTGGCAAGCAGCTGGACCAGCAGCGCTCCAGC 3744
QY 1121 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArg 1140
Db 3745 AGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGGAGAGAGCCGAGCGGGAGCGGAGG 3804
QY 1141 SerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAsp 1160
Db 3805 TCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGATGAGAGGAAAGTTTCAGAAAGGAC 3864
QY 1161 ArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLys 1180
Db 3865 CGGGCCAGCCAGCAGGAGTACCATCGCCACAGGGGTTCCTTGGAACTGTAGGCCAAG 3924
QY 1181 SerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGly 1200
Db 3925 AGTTCCTTTGACCTGCCTGACACTCTGCAGGTCCGGGGCTGCACCGCACAGCCAGCGC 3984
QY 1201 ArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1220
Db 3985 CGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTCAGGGCGTTTGCC 4044
QY 1221 ArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsn 1240
Db 4045 CGCACCCCTGAGGACTGATGATGCCCAACTGGATGGGGATGATGACAAATGATGAGGGAAT 4104
QY 1241 LeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArg 1260
Db 4105 CTGAGCAAGGGGAACGCATACAAGCCTGGGTGAGATCCCGGCTTCCTGCCTGTTGCCGA 4164
QY 1261 GluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCys 1280
Db 4165 GAGCGAGATTCTGGTCGGCTATATCTTCTCCTCAGTCAAGGTTTCGTCTCCTGTGT 4224
QY 1281 HisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsn 1300
Db 4225 CACCGGATCATCACCCACAAGATGTTTGACCATGTGGTCTCTGTCATCATCTTCCTCAAC 4284
QY 1301 CysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePhe 1320
Db 4285 TGTATCACCATCGTATGGAGCGCCCCAAAATTGACCCCCACAGCGCTGAGCGCATCTTC 4344
QY 1321 LeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysVal 1340
Db 4345 CTGACCCCTCTCCAACTACATCTTCACGGCAGTCTTTCTAGCTGAAATGACAGTGAAGTG 4404
QY 1341 ValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeu 1360
Db 4405 GTGGCACTGGGCTGGTGTCTTGGGAGCAGGCCCTACCTGCGCAGCAGCTGGAATGTGCTG 4464
QY 1361 AspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSer 1380
Db 4465 GACGGCTTGTGGTGTCTCATCTCCGTTCATCGACATCTCCTGCTCCTATGGTCTCCGACAGC 4524
QY 1381 GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeu 1400
Db 4525 GGCACCAAGATCCTTGGCATGTGTAGGGTGTGTGGGCTGTGTGGGACCCCTGCGTCCACTC 4584
QY 1401 ArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeu 1420
Db 4585 AGGGTCATCAGCCGGGCCAGGAGCTGAAGCTGGTGGTAGAGACTCTGTATGTCTATCCCTC 4644
QY 1421 LysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeu 1440

Db	4645	AAACCCATTGGCAACATTGTGGTCAATTTGCTGTGCTCTTCTTCATCATTTTGTGAATTCTC	4704
QY	1441	GlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIle	1460
Db	4705	GGGGTGCAGCTCTTCAAAGGAAGTTCTTCGTGTGTGAGGTGAGGACACAGGAACATC	4764
QY	1461	ThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPhe	1480
Db	4765	ACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGGCAACAAGTACAACTTT	4824
QY	1481	AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal	1500
Db	4825	GACAAACCTGGGCCAGGCTCTGATGTCCCTGTTGTGTGCTGGCTCCAAAGGATGGTTGGGTT	4884
QY	1501	AspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHis	1520
Db	4885	GACATCATGTATGATGGCTGGATGCTGTGGGTGTGGATCAGCAGCCCATCATGAACCCAC	4944
QY	1521	AsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeu	1540
Db	4945	AAACCCCTGGATGCTGTACTTTCATCTCCTTCTCCTCATCGTGGCTTCTTTGTCTCTG	5004
QY	1541	AsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGlu	1560
Db	5005	AACATGTTTGTGGGCGTGGTGGAGAACTTCCATAAGTGCAGACAGCACAGGAGGAG	5064
QY	1561	GluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSer	1580
Db	5065	GAGGAGCGGAGCGCGGTGAGGAGAACGACTACGGAGGCTGGAGAAAAAGAGAAGGAGT	5124
QY	1581	LysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1600
Db	5125	AAGGAGAAGCAGATGGCCGAAGCCAGTGCAGGCCCTACTACTCTGACTACTCGAGATTCTC	5184
QY	1601	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1620
Db	5185	CGGCTCCTTGTCCACCACCTGTGTACCAAGCCACTACCTGGACCTCTTTCATCTGCTGTC	5244
QY	1621	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1640
Db	5245	ATCGGGCTGAACGTGCTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGAC	5304
QY	1641	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPhe	1660
Db	5305	GAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTTTGTCTTTGAGTCAGTTTTC	5364
QY	1661	LysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1680
Db	5365	AAACTTGTGGCCTTTGGGTTCCGCGTTTCTTCCAGGACAGGTGGAAACCAGCTGGACCTG	5424
QY	1681	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsnLeuSer	1700
Db	5425	GCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTCTG	5484
QY	1701	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1720
Db	5485	CTGCCCATCAACCCCAACCATCATCCGTATCATGAGGGTGTCCCGCATTTGCTCGAGTTCTG	5544
QY	1721	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeu	1740
Db	5545	AAGCTGTTGAAGATGGCTGTGGGATGCGGGCATCTGCTGCACACGGTGATGCAGGCCCTG	5604
QY	1741	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1760
Db	5605	CCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTTTCATCTTTTGCAGCTCTG	5664
QY	1761	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1780
Db	5665	GGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGGGT	5724
QY	1781	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1800

Db	5725	CGSCATGCCACCTTTAGGAACCTTTGGTATGGCCCTTTCTGACCCCTCTTCCGAGTCTCCACT	5784
Qy	1801	GlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThr	1820
Db	5785	GGTGACAACTGGAATGGTATTATGAAGGACCCCTTCCCGGACTGTGACCAGGAGTCCACC	5844
Qy	1821	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1840
Db	5845	TGCTACAACACTGTCTCATCTCCCTATCTACTTTGTGTCTTTCGTGCTGACGGCCAGTTT	5904
Qy	1841	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1860
Db	5905	GTGCTGGTCAACGCTGGTTCATAGCTGTGTGATGAAGCACCTGGAAGAAAGCAACAAGAG	5964
Qy	1861	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro	1880
Db	5965	GCCAAAGGAGGAGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCG	6024
Qy	1881	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSer	1900
Db	6025	CAGCCCCACTCCCCGCTGGGCAGCCCTTCTCTGGCCCCGGGTGGAGGGTGTCAACAGT	6084
Qy	1901	ThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGly	1920
Db	6085	ACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTTGGAGCAGCCTCGGGC	6144
Qy	1921	PheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGly	1940
Db	6145	TTCTCCCTTGAGCACCCACCGATGGTATCCCCACCCGAGGAGGTGCCAGTCCCCCTAGGA	6204
Qy	1941	ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAsp	1960
Db	6205	CCAGACCTTGCTGACTGTAGGAAGTCTGGTGTGAGCCGGACGCCACTCTCTGCCCAATGAC	6264
Qy	1961	SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGly	1980
Db	6265	AGCTACATGTGCGGCAATGGGAGCACTGCTGAGAGATCCCTTAGGACACAGGGGCTGGGG	6324
Qy	1981	LeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSer	2000
Db	6325	CTCCCCAAAGCCAGTCAGGCTCCATCTGTTCGGTTACCTCCCAACCAGCAGACACCAGC	6384
Qy	2001	CysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThr	2020
Db	6385	TGCATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGCTCACCACC	6444
Qy	2021	TrpGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeu	2040
Db	6445	TGGGGGGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCCTCTGGCTCAGAGGCCTCTC	6504
Qy	2041	ArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu	2060
Db	6505	AGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGACGGGCCTGGGTAGCCGGAA	6564
Qy	2061	AspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrp	2080
Db	6565	GACCTGTGTGACAGGTGAGTGGGCCCTCCTGCCCTCTGACCCCGTCTCATCTTCTGG	6624
Qy	2081	GlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHis	2100
Db	6625	GGCGGGTGCAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAAGCAC	6684
Qy	2101	IleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGlu	2120
Db	6685	ATCCGCCTGCCAGCCCTTGGCCAGGCCCTGGAACCCAGCTGGGCCAAGGACCCCTCCAGAG	6744
Qy	2121	ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro	2140
Db	6745	ACCAGAAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTTCAGGAGACCTCTCTCC	6804
Qy	2141	SerSerGlnGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThr	2160
Db	6805	AGCAGCCAGGAAGAACCCCTGTTCCCAACCGGACCTGAAGAAGTGTCTACAGTGTAGAGACC	6864

Db 256 CGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTTTCTTCTACTTGAGCCAGGACA 315
QY 100 eArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerM 120
Db 316 GCCGCCGGGAGCTGGTGTCTCCGACGGTCTGTAAACCCGTGGTTCGAGCGAGTCAGTA 375
QY 120 etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA 140
Db 376 TGCTGGTCAATCTTCTCAACTGTGTGACTCTGGGTAATGTTTCAGGCCGTGTGAGGACATTG 435
QY 140 laCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPheP 160
Db 436 CCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCCTTCGATGACTTTCATCTTTGCCCTTCT 495
QY 160 heAlaValGluMetValValIysMetValAlaLeuGlyIlePheGlyLysCysTyrL 180
Db 496 TTGCTGTGGAATGGTGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAGAAATGTTACC 555
QY 180 euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200
Db 556 TGGGAGACACTTGGAAACCGCTTGACTTTTTCATTGTTCATTGCAGGGATGCTGGAGTATT 615
QY 200 erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL 220
Db 616 CGCTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGGACAGTCCGTGTGCTGGACCGC 675
QY 220 euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL 240
Db 676 TCAGGGCCATTAAACCGGTGCCAGCATGCGCATTTCTCGTCACATTACTGTGGACACCT 735
QY 240 euProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIleGlyIleV 260
Db 736 TGCCATATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTCTCGTCTTTTTCATCTTTGGCATCG 795
QY 260 alGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheS 280
Db 796 TGGGCGTCCAGCTGTGGCAGGACTGCTTCGCAACCGGTGCTTCTCCCGGAGAACTTCA 855
QY 280 erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP 300
Db 856 GCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAAATGAGGACGAGAGCC 915
QY 300 roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL 320
Db 916 CCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGAGATCCTGCAGGAGTGTGCCACAC 975
QY 320 euArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS 340
Db 976 TGCCTGGGGAAGGCGGTGGTGGCCCCCCTGCAGTCTGGACTATGAGACCTATAACAGTT 1035
QY 340 erSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH 360
Db 1036 CCAGCAACACCACTGTGTCAACTGGAAACAGTACTATACCAACTGCTCTGCGGCGGAGC 1095
QY 360 isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP 380
Db 1096 ACAACCCCTTCAAAGCGGCCATCACTTTGACAAACATTGGCTATGCTTGGATCGCCATCT 1155
QY 380 heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisS 400
Db 1156 TCCAGGTTCATCACACTGGAGGGCTGGTGCACATCATGTACTTCGTAATGGACGCTCACT 1215
QY 400 erPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleA 420
Db 1216 CCTTCTACAACTTCATCTACTTTCATCTTCTCATCATCGTGGGCTCCTTCTTCATGATCA 1275
QY 420 snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL 440
Db 1276 ACCTGTGCCTGGTGGTGTATGCCCACGAGTTCTCCGAGACCAACAGCGGAGAGTCAGC 1335
QY 440 euMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG 460
Db 1336 TGATCGGGGAGCAGCGGTGTACGATTCTCTGTCCAATGTCTAGCACCCCTGGCAAGCTTCTCTG 1395

QY 460 luProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaA 480
Db 1396 AGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCTCCGAAAAGCAG 1455
QY 480 laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP 500
Db 1456 CCCGAAGGCTGGCCCGAGTCTCTAGGGCTATAGGCGTGGGGCTGGGCTGCTCAGCAGCC 1515
QY 500 roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA 520
Db 1516 CAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTCAGTCAGCTGCACCTCGCTCACACCGTC 1575
QY 520 rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisLeuG 540
Db 1576 GTCTGTCTGTCCACCACCTGGTCCACCACCATCACACCATCACACCTACACCTGG 1635
QY 540 lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560
Db 1636 GTAATGGGACGCTCAGAGTCCCCGGGCCAGCCAGAGATCCAGGACAGGATGCCAATG 1695
QY 560 lySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA 580
Db 1696 GGTCTCGCCGGTCTCATGTACCACACCCCTCTACACCCACTCCCTCTGGGGGCCCTCCGA 1755
QY 580 rgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC 600
Db 1756 GGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCGTT 1815
QY 600 ysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
Db 1816 GCCAGGCACCCCTCCAGATGCCATCGGAGGCATCTGGTAGACTTGGGTAGTGGGA 1875
QY 620 ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV 640
Db 1876 AGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAGATACTGAAGGATAAAGCACTAG 1935
QY 640 alGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyP 660
Db 1936 TGGAGTGGCCCCCAGCCCTGGGCCCCCCCCACCCCTCACAGCTTCAACATCCCACCTGGGC 1995
QY 660 roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC 680
Db 1996 CCTTCAGTCCATGCACAAGCTCCTGGAGACACAGAGTACGGGAGCCTGCCATAGTCTCCT 2055
QY 680 ysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP 700
Db 2056 GCAAAATCTCCAGCCCTTGTCTCAAAGGCAGACAGTGGAGCCTCGGGCCGGACAGTTGTC 2115
QY 700 roTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspS 720
Db 2116 CCTACTGTCCCCGACAGGAGCAGGAGAGCCAGAGTCCGCTGACCATGTCTGCTGACT 2175
QY 720 erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspP 740
Db 2176 CAGACAGCGAGGCTGTGTATGAGTTCAACAGGACGCTCAGCACAGTGACCTCCGGGATC 2235
QY 740 roHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA 760
Db 2236 CCCACAGCCGGCGGCAGACGGAGCCCTGGGCCCCAGATGCAGAGCCTAGTTCTGTGCTGG 2295
QY 760 laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA 780
Db 2296 CTTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATCGTAGATAGCAAAATACTTTGGCC 2355
QY 780 rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800
Db 2356 GGGGAATCATGATCGCCATCCTCGTCAATACACTCAGCATGGGCATCGAGTACCAGCAGC 2415
QY 800 lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820
Db 2416 AGCCCGGAGAGCTCACCAACGCCCTTGGAAATCAGAAATCAGAAACATCGTCTTTCACCGCCTCTCG 2475

QY 820 laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840
DB 2476 CCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTTGGCTACATTAAAGAAATCCCT 2535
QY 840 yrAsnIlePheAspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnG 860
DB 2536 ACAACATCTTTGATGGTGTCAATTGTGTGTCATCAGTGTGTGGGAGATTGTGGCCAGCAGG 2595
QY 860 lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgp 880
DB 2596 GAGGTGGCCTGTCCGTGCTGCGGACCTTCCGCCTGATGCGGGTGTGAAGCTGGTGGCT 2655
QY 880 heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT 900
DB 2656 TCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATGAAGACCATGGACAAACGTGGCCA 2715
QY 900 hrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeup 920
DB 2716 CCTTCTGCATGCTCCTCATGTGTTCATCTTTCATCTTTCAGCATCTTGGGCATGTCATCTCT 2775
QY 920 heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 940
DB 2776 TTGGTTGCAAGTTCCCATCTGAACGGGATGGGACACGTTGCCAGACCCGGAAGAAATTCG 2835
QY 940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAsnL 960
DB 2836 ACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATTCTGACTCAGGAAGACTGGGAATA 2895
QY 960 ysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAlaAlaLeuTyrPheIleAlaL 980
DB 2896 AAGTCCTCTACAAACGGCATGGCCTCCACATCGTCTTGGGCTGCTTTTACTTTCATCGCCC 2955
QY 980 euMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP 1000
DB 2956 TCATGACTTTTGGCAACTATGTGTCTCTTTAAACCTGCTGGTGGCCATCTTGTGGAAGGAT 3015
QY 1000 heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV 1020
DB 3016 TCCAGGCAGAGGGAGATGCCAACGCTGAGTCAGAGCCCTGATTTCTTTTCGCCCCAGTG 3075
QY 1020 alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG 1040
DB 3076 TGGATGGTGTATGGGGACAGAAAGACGCTTGGCCCTGTTGGCTTTGGGAGAACACGCGG 3135
QY 1040 luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH 1060
DB 3136 AACTACGAAAGAGCCTTTTGGCACCCCTCATCATCCATACGGCTGGGACACCAATGTAC 3195
QY 1060 isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrS 1080
DB 3196 ACCCCAAGAGCTCCAGCACAGGTGTGGGGAAGCACTTGGGCTCTGGCTCTCGACGTACCA 3255
QY 1080 erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSera 1100
DB 3256 GTAGCAGTGGTCCGCTGAGCCTGGAGCTGGCCACCATGAGATGAAATGTCCGCCAAGTG 3315
QY 1100 laArgSerSerProHisSerProTyrSerAlaAlaSerSerTyrThrSerArgArgSerS 1120
DB 3316 CCCGCAGCTCCCCCGCACAGTCCCTGGAGTGGGCAAGCAGCTGGACCCAGCAGGCGCTCCA 3375
QY 1120 erArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgA 1140
DB 3376 GCAGGAACAGCCTGGGCCGGGGCCCCCAGCCTAAAGCGGAGGAGCCCGAGGGGAGCGGA 3435
QY 1140 rgSerLeuLeuSerGlyGluGlyGlnGlnSerGlnAspGluGluSerSerGluGluA 1160
DB 3436 GGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAAGTTTCAGAAAGG 3495
QY 1160 spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluGluAlaL 1180
DB 3496 ACCGGGCCAGCCCGCAGGCAGTGACCATCGCCACAGGGGTTCTTGGAAACGTGAGGCCA 3555
QY 1180 ysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG 1200

DB 3556 AGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCGGGGCTGCACCGCACAGCCAGCG 3615
QY 1200 lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
DB 3616 GCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTCAGGGCGTTTGG 3675
QY 1220 laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyA 1240
DB 3676 CCCGCACCTTGAGGACTGATGACCCCAACTGGATGGGATGATGACAATGATGAGGGAA 3735
QY 1240 snLeuSerLysGlyGluArgIleGlnAlaTyrValArgSerArgLeuProAlaCysCysA 1260
DB 3736 ATCTGAGCAAAAGGGGAACGCATACAAGCCTGGGTTCAGATCCCGGCTTCTGCCTGTTGCC 3795
QY 1260 rgGluArgAspSerTyrSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuC 1280
DB 3796 GAGAGCGAGATTCTGTGTCGGCCTATATCTTTCCTCCTCAGTCAAGGTTTCGTCTCCTGT 3855
QY 1280 ysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA 1300
DB 3856 GTCACCGGATCATCCCCACAAGATGTTTGACCATGTGGTCTCTCGTCATCATCTTCTCTCA 3915
QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
DB 3916 ACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGACCCACAGCGCTGAGCGCATCT 3975
QY 1320 heLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
DB 3976 TCCTGACCTCTCCAACACTACATCTTCACGGCAGTCTTTCTAGCTGAAATGACAGTGAAG 4035
QY 1340 alValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTyrAsnValL 1360
DB 4036 TGGTGGCACTGGGCTGGTGTCTTGGGAGCAGGCCCTACCTGCAGCAGCTGGAATGTGC 4095
QY 1360 euAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsps 1380
DB 4096 TGGACGGCTTGTGGTGTCTCATCTCCGTTCATCGACATCCTGGTTCCTCATGGTCTCCGACA 4155
QY 1380 erGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProL 1400
DB 4156 GCGGCACCAAGATCCTTGGCATGCTGAGGGTGTGCGGCTGTGGGACCCCTGCGTCCAC 4215
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL 1420
DB 4216 TCAGGGTTCATCAGCCGGGCCAGGACTGGAAGCTGGTGTAGAGACTCTGATGTATCCTCC 4275
QY 1420 euLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleL 1440
DB 4276 TCAAAACCCATTGGCAACATTTGTGTCAATTGTGTGCTTCTTCTCATCATTTTGGAAATTC 4335
QY 1440 euGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnI 1460
DB 4336 TCGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGTAGGGTGTAGGACACCCAGGAACA 4395
QY 1460 leThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsnP 1480
DB 4396 TCACTAAACAAATCCGACTGGCTGAGCCAGCTACCGATGGGTCCGGCACAAGTACAACT 4455
QY 1480 heAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrP 1500
DB 4456 TTGACAAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTGTGGCTCCAAGGATGGTTGGG 4515
QY 1500 alAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH 1520
DB 4516 TTGACATCATGTATGATGGGCTGGATGTGTGGTGTGGATCAGCAGCCCATCATGAACC 4575
QY 1520 isAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValL 1540
DB 4576 ACAACCCCTGGATGCTGTATACTTTCATCTCCTTCTCCTCATCGTGGCCTTCTTTGTCC 4635
QY 1540 euAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluG 1560

Db	4636	TGAACATGTTTGTGGCGTGGTGGAGAACTTCCATAAGTGCAGACAGCACCGAGG	4695
QY	1560	luGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgS	1580
Db	4696	AGGAGAGCGAGCGCGGTGAGGAGAGCGACTACGGAGGCTGGAGAAAAAGAGAGGA	4755
QY	1580	erLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgP	1600
Db	4756	GTAAGAGAAGCAGATGGCCGAAGCCAGTGCAAGCCCTACTACTCTGACTACTCGAGAT	4815
QY	1600	heArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyV	1620
Db	4816	TCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTG	4875
QY	1620	alileGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA	1640
Db	4876	TCATCGGCTGAACGTGGTCACTATGGCCATGGACATTACCAGCAGCCCCAGATCCTGG	4935
QY	1640	spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP	1660
Db	4936	ACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTGATCAGTTT	4995
QY	1660	heLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspL	1680
Db	4996	TCAAACCTTGTGGCCTTTGGCTTCGCGCTTTCTTCCAGACAGGTGGAAACCAGCTGGACC	5055
QY	1680	euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS	1700
Db	5056	TGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGT	5115
QY	1700	erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL	1720
Db	5116	CGCTGCCCATCAACCCCAACCATCATCCGTATCATGAGGTGCTCCGCATTGCTCGAGTTC	5175
QY	1720	euLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL	1740
Db	5176	TGAAGCTGTTGAAGATGGCTGTGGGCATCGGGCACTGCTGCACACGGTGATGCAGGCC	5235
QY	1740	euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL	1760
Db	5236	TGCCCCAGGTGGGAAACCTGGGACITCTCTCATGTTATTGTTTTCATCTTTGCAGCTC	5295
QY	1760	euGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG	1780
Db	5296	TGGGCGTGGAGCTCTTTGGAGACCCTGGAGTGTATGAGACACACCCCTTGTGAGGGCTTG	5355
QY	1780	lyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT	1800
Db	5356	GTCCGCATGCCACCTTTAGGAACTTTGGTATGGCCCTTTCTGACCCCTCTTCCGAGTCTCCA	5415
QY	1800	hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT	1820
Db	5416	CTGGTGACAACCTGGAATGGTATTATGAGGACACCCCTCCGGGACTGTGACCAGGATCCA	5475
QY	1820	hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP	1840
Db	5476	CCTGCTACAACACTGTCTATCTCCCTATCTACTTTGTGTCTCTTGTGCTGACGGCCAGT	5535
QY	1840	heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysG	1860
Db	5536	TTGTGCTGGTCAACGTGTCTAGCTGTGTGATGAGCACCTTGAAGAAAGCAACAAAG	5595
QY	1860	luAlaLysGluGluAlaGluLeuAlaGluLeuGluLeuGluMetLysThrLeuSerP	1880
Db	5596	AGGCCAAGGAGGAGCGCAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCC	5655
QY	1880	roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS	1900
Db	5656	CGCAGCCCCACTCCCCGCTGGGCAGCCCCCTTCTCTGGCCCCGGGTGGAGGGTGTCAACA	5715
QY	1900	erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG	1920
Db	5716	GTA CTGACAGCCCTAAGCCCTGGGGCTCCACACCACTGCCCCACATTGGAGCAGCCTCG	5775

QY	1920	lyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG	1940
Db	5776	GCTTCTCCTTGAGCACCCACGATGGTACCCACCCCGAGGAGGTGCCAGTCCCCCTAG	5835
QY	1940	lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA	1960
Db	5836	GACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTTCAGCGGACGCACCTCTCTGCCCAATG	5895
QY	1960	spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG	1980
Db	5896	ACAGCTACATGTCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGG	5955
QY	1980	lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS	2000
Db	5956	GGCTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCAGCAGACACCA	6015
QY	2000	erCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProT	2020
Db	6016	GCTGCATCCTACAGCTTCCCAAAGATGTGCACATACTGTCTCCAGCCTCATGGGCTCCCA	6075
QY	2020	hrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProL	2040
Db	6076	CCTGGGCGCCATCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGGCCTC	6135
QY	2040	euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG	2060
Db	6136	TCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGCGCTGGGTAGCCGGG	6195
QY	2060	luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT	2080
Db	6196	AAGACCTGTTGTACAGAGTGAGTGGGCCCTCTCTGCCCTCTGCACCGGTCTCATCTCTCT	6255
QY	2080	rpGlyGlySerSerIleGlnValGlnArgSerGlyIleGlnSerLysValSerLysH	2100
Db	6256	GGGCGGGTTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAGC	6315
QY	2100	isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG	2120
Db	6316	ACATCCGCTGCCAGCCCTTGCCAGGCCTGGAACCCAGCTGGGCCAAGGACCTCCAG	6375
QY	2120	luThrArgSerSerLeuLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeup	2140
Db	6376	AGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGTGGATTTTCAGGAGACCTCTCTC	6435
QY	2140	roSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluT	2160
Db	6436	CCAGCAGCCAGGAAGAACCCCTGTTCCACCGGACCTGAAGAAGTGTACAGTGTAGAGA	6495
QY	2160	hrGlnSerCysArgArgArgProGlyPheThrLeuAspGluGlnArgArgHisSerIleA	2180
Db	6496	CCCAGAGCTGCAGCGCAGGCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTG	6555
QY	2180	laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG	2200
Db	6556	CTGTCACTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCG	6615
QY	2200	lyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerI	2220
Db	6616	GGGGCCAACTCTTGGGGGTCTGGGAGCCGGCCTTAAGAAAAAACTCAGCCCAACCCAGTA	6675
QY	2220	leSerIleAspProProGluSerGlnGlySerArgProLysLysLysLeuSerProGlyValCysL	2240
Db	6676	TCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCTCTGGTGTCTGCC	6735
QY	2240	euArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAsps	2260
Db	6736	TCAGGAGGAGGGCGCCGCGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCTTGACA	6795
QY	2260	erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerA	2280
Db	6796	GCACGGCTGCCTCACCTTCCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTCTG	6855

QY	180	euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS	200	QY	540	lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG	560
Db	925	TGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTTCATTGCAGGGATGCTGGAGTATT	984	Db	2005	GTAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGGACAGGGATGCCAATG	2064
QY	200	erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL	220	QY	560	lySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA	580
Db	985	CGCTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGGACAGTCCGTGTGCTGCGACCGC	1044	Db	2065	GGTCTCGCGGCTCATGCTACCAACCACCTCTACACCCACTCCCTCTGGGGCCCTCCGA	2124
QY	220	euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL	240	QY	580	rgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC	600
Db	1045	TCAGGGCCATTAAACCGGTGCCAGCATGCCAATTCCTGTCATCTTTTTCATCTTTGGCATCG	1104	Db	2125	GGGTGCGGAGTCTGTACACAGCTTCTACCATGTGACTGCCACTTGGAGCCAGTCCGTT	2184
QY	240	euProMetLeuGlyAsnValLeuLeuLeuCysPheValPhePheIlePheGlyIleV	260	QY	600	ysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL	620
Db	1105	TGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTCGTCTTTTTCATCTTTGGCATCG	1164	Db	2185	GCCAGGACACCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGGGA	2244
QY	260	alGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheS	280	QY	620	ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV	640
Db	1165	TGGGCGTCCAGCTGTGGCAGGACTGCTTCGCAACCGGTGCTTCCTCCCGAGAACTTCA	1224	Db	2245	AGGTGTACCCCACTGTGCATACCAAGCCCTCCAGAGATCTGAAGGATAAAGCACTAG	2304
QY	280	erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP	300	QY	640	alGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP	660
Db	1225	GCTTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAAATGAGACGAGGCC	1284	Db	2305	TGGAGGTGGCCCCAGCCCTGGGCCCCCACCCTCACAGCTTCAACATCCCACCTGGGC	2364
QY	300	roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL	320	QY	660	roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC	680
Db	1285	CCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGGATCCTGCAGGAGTGTGCCACAC	1344	Db	2365	CCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTACGGGAGCCTGCCATAGCTCCT	2424
QY	320	euArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS	340	QY	680	ysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP	700
Db	1345	TGCGTGGGGAAGCGGTGGTGGCCCCACCTGCAGTCTGGAATATGAGACCTATAACAGTT	1404	Db	2425	GCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCCTGCGGGCCGGACAGTTGTC	2484
QY	340	erSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH	360	QY	700	roTyrCysAlaAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspS	720
Db	1405	CCAGCAACACCACCTGTGTCAACTGGAACCACTACTATACCAACTGCTCTGCGGGCGAGC	1464	Db	2485	CCTACTGTGCCCGACAGGAGCAGGAGCCAGAGTCCGCTGACCATGTTCATGCCTGACT	2544
QY	360	isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP	380	QY	720	erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspP	740
Db	1465	ACAAACCCCTTCAAAGGCGCCATCAACTTTGACAACTTGGCTATGCCTGGATCGCCATCT	1524	Db	2545	CAGACAGCGAGGCTGTGTATGAGTTTCACACAGGACGCTCAGCACAGTACCTCCGGGATC	2604
QY	380	heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisS	400	QY	740	roHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA	760
Db	1525	TCCAGGTTCATCACACTGGAGGGCTGGGTCCGACATCATGTACTTCGTAATGGACGCTCACT	1584	Db	2605	CCACAGCCGGCGGACAGCGGAGCCCTGGGCCCAGATGCAGAGCCCTAGTTCTGTGTGG	2664
QY	400	erPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA	420	QY	760	laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA	780
Db	1585	CCTTCTACAACCTCATCTACTTCAATCTCTTCATCATCGTGGGCTCCTTCTTCATGATCA	1644	Db	2665	CTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATCGTAGATAGCAAAATACTTTGGCC	2724
QY	420	snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL	440	QY	780	rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG	800
Db	1645	ACCTGTGCCTGGTGTGATTGCCACGCAGTTCCTCGAGACCAACAGCGGGAGAGTCAGC	1704	Db	2725	GGGGAATCATGATCGCCATCCTGGTCAATACACTCAGCATGGGCATCGAGTACCACGAGC	2784
QY	440	euMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG	460	QY	800	lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA	820
Db	1705	TGATCGGGGAGCAGCGTGTACGATTCTGTCCAATGTAGCACCTTGGCAAGCTTCTCTG	1764	Db	2785	AGCCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTTACCAGCCTCTTCG	2844
QY	460	luProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaA	480	QY	820	laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT	840
Db	1765	AGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCCTCCGAAAAGCAG	1824	Db	2845	CCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTTGGCTACATTAGAATCCCT	2904
QY	480	laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP	500	QY	840	yrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnG	860
Db	1825	CCCGAAGGCTGGCCCCAGGTCTCTAGGGCTATAGGCGTGGGGCTGGGCTGCTCAGCAGCC	1884	Db	2905	ACAACATCTTTGATGGTGTCTATTGTGGTTCATCAGTGTGGGAGATTGTGGGCCAGCAGG	2964
QY	500	roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA	520	QY	860	lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP	880
Db	1885	CAGTGGCCCCGTAGTGGGCAGGAGCCCCAGCCAGTCAGTCAGCTCGCTCACACCGTGC	1944	Db	2965	GAGGTGGCCTGTCCGTGCTCGGACCTTCCGCCCTGATCGGGTGTGAAGCTGGTGCCT	3024
QY	520	rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuG	540	QY	880	heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT	900
Db	1945	GTCTGTCTGTCCACCACCTGGTCCACCACCATCACACCACCATCACACTACCCACTGG	2004	Db	3025	TCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATGAAGACCATGGACACCGTGGCCA	3084
				QY	900	hrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuP	920

Db 3085 CCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTCAGCATCCTGGGCATGCATCTCT 3144
QY 920 heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 940
Db 3145 TTGGTTGAAGTTCCGATCTGAAAGGATGGGACACGTTGCCAGACCCGGAAGAAATTTCG 3204
QY 940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL 960
Db 3205 ACTCCCTGCTGGGCCATCGTCACTGCTCTTTACAGATTCTGACTCAGGAAGACTGGAATA 3264
QY 960 ysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaL 980
Db 3265 AAGTCCCTTACAAACGGCATGGCCCTCCACATCGTCTTTGGGCTGCTCTTTACTTCATCGCCC 3324
QY 980 euMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyP 1000
Db 3325 TCATGACTTTTGGCAACTATGTGCTCTTTAACTGCTGGTGGCCATTCTTTGTGAAGGAT 3384
QY 1000 heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV 1020
Db 3385 TCCAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGAGCTGATTTCTTTTCGCCCAGTG 3444
QY 1020 alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG 1040
Db 3445 TGGATGGTGATGGGGACAGAAAGACGCTTGGCCCTGGTGGCTTTGGGAGAACACGCGG 3504
QY 1040 luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH 1060
Db 3505 AACTACGAAAGAGCCTTTTGGCACCCCTCATCATCCATCAGGCTGCGACACCAATGTAC 3564
QY 1060 isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrs 1080
Db 3565 ACCCCAAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTGGGCTCTGGCTCTCGACGTACCA 3624
QY 1080 erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerA 1100
Db 3625 GTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAAATGTCCGCCAAGTG 3684
QY 1100 laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerS 1120
Db 3685 CCCGAGCTCCCGCACAGTCCCTGGAGTGGGCAAGCAGCTGGACCAGCAGCGCTCCA 3744
QY 1120 erArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgA 1140
Db 3745 GCAGGAACAGCCTGGGCCGGGCCCGCCAGCCTAAAGCGGAGGAGCCCGAGCGGAGCGGA 3804
QY 1140 rgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluA 1160
Db 3805 GGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAGTTCAGAAGAGG 3864
QY 1160 spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL 1180
Db 3865 ACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGGGGTTCTTTGGAACGTGAGGCCA 3924
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Db 3925 AGAGTTCTTTGACCTGCCTGCACACTCTGCAGGTGCCGGGGCTGCACCGCACAGCCAGCG 3984
QY 1200 lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
Db 3985 GCCGGAGCTCTGCCCTCTGAGCACCAAGACTGTAATGGCAAGTCCGGCTTCAGGGCGTTTGG 4044
QY 1220 laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyA 1240
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Db 4165 GAGAGCGAGATTCTCTGGTCGGCCTATATCTTTCTCTCCTCAGTCAAGGTTTCTGCTCCTGT 4224
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Db 4225 GTCACGGATCATCACCCACAAGATGTTTGACCATGTGGTCTCGTTCATCATCTCTCCTCA 4284
QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
Db 4285 ACTGTATCACCATCGCTATGAGCGCCCCAAATATGACCCCCACAGCGCTGAGCGCATCT 4344
QY 1320 heLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
Db 4345 TCCTGACCCCTCTCCAACCTACATCTTCACGGCAGTCTTTCTAGCTGAAATGACAGTGAAGG 4404
QY 1340 alValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValL 1360
Db 4405 TGGTGGCACTGGGCTGGTGGTTGGGAGCAGGGCTACCTGGCAGCAGCTGGAATGTGC 4464
QY 1360 euAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsps 1380
Db 4465 TGGACGGCTTGTGGTGTCTCATCTCCGTTCATCGACATCTCGGTCTCCATGGTCTCCGACA 4524
QY 1380 erGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProL 1400
Db 4525 GCGGCACCAAGATCCTTGGCATGCTGAGGGTGTCTGCGGTGTCTGCGGACCCCTGCGTCCAC 4584
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL 1420
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QY 1420 euLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleL 1440
Db 4645 TCAAAACCCATTGGCAACATTGTGGTCAATTTGTGTGGCTTCTTCATCATTTTTTGGAAATTC 4704
QY 1440 euGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnI 1460
Db 4705 TCGGGGTGCAGCTCTTCAAAAGGAAAGTTCTTCGTGTGTCTCAGGGTGAGGACACCAGGAACA 4764
QY 1460 leThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnP 1480
Db 4765 TCACCTAAACAAATCCGACTGGCTGAGGCCAGCTACCGATGGGTCCGGCACAAAGTACAAC 4824
QY 1500 alAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH 1520
Db 4885 TTGACATCATGTATGATGGGCTGGATGCTGTGGGTGGATCAGCAGCCCCATCATGAACC 4944
QY 1520 isAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValL 1540
Db 4945 ACAACCCCTGGATGTGTATCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5004
QY 1540 euAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluG 1560
Db 5005 TGAACATGTTTGTGGCGGTGGTGGAGAACTTCCATAAGTGCAGACAGCAGCAGGAGG 5064
QY 1560 luGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgS 1580
Db 5065 AGGAGGAGCGAGCGCGCTGAGGAGAAGCGACTACGAGGGCTGGAGAAAAGAGAAAGGA 5124
QY 1580 erLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgP 1600
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Db 5185 TCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTTCATCACTGGTG 5244
QY 1620 alIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA 1640
Db 5245 TCATCGGGCTGAACGTGGTCACTATGGCCATATGGCAACATTACCAGCAGCCCCCAGATCCTGG 5304

QY 1640 spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP 1660
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QY 1660 heLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspL 1680
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QY 1680 euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS 1700
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QY 1700 erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL 1720
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QY 1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT 1820
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Db 6265 ACAGCTACATGTGCCCAATGGGAGCACTGTGAGAGATCCCTAGGACACAGGGGCTGGG 6324
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QY 2020 hrTrpGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProL 2040
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QY 2060 luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT 2080
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QY 2080 rpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysH 2100
Db 6625 GGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAGC 6684
QY 2100 isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG 2120
Db 6685 ACATCCGCTGCCAGCCCTTTGCCCAGGCCTGGAACCCAGCTGGCCAAAGGACCTCCAG 6744
QY 2120 luThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuP 2140
Db 6745 AGACCAGAAGCAGCTTAGAGCTGCACACGGAGCTGAGCTGAGTTTCAGGAGACCTCCTTC 6804
QY 2140 roSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluT 2160
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Db 6925 CTGTCACTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCG 6984
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QY 2220 leSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysL 2240
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QY 2240 euArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAsps 2260
Db 7105 TCAGGAGGAGGGCGCGCCAGTACTCTTAAGGATCCCTCGGTCTCCAGCCCCCTTGACA 7164
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QY 2280 spProThrAspMetAspPro 2286
Db 7225 ACCCAACAGACATGGACCCC 7244

RESULT 4
BD224079 7285 bp DNA linear PAT 17-JUL-2003
LOCUS BD224079
DEFINITION T-type calcium channel.
ACCESSION BD224079
VERSION BD224079.1 GI:33033849
KEYWORDS JP 2002525077-A/2.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 7285)

AUTHORS Li,M.
TITLE T-type calcium channel
JOURNAL Patent: JP 2002525077-A 2 13-AUG-2002;
SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION
COMMENT OS Rattus sp. (rat)
PN JP 2002525077-A/2
PD 13-AUG-2002
PF 26-AUG-1999 JP 2000570372
PR 26-AUG-1998 US 60/098004,27-JAN-1999 US 60/117399 PI
MING LI
PC C12N15/09,A61K31/711,A61K45/00,A61K48/00,A61P3/10,C07K14/47,
C07K16/18,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/68,G01N33/
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C12P21/08,
PC C12N15/00,C12N5/00
CC T-type calcium channel
FH Key Location/Qualifiers
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FT /organism='Rattus sp. (rat)'.
FT /mol_type='genomic DNA'
FT /db_xref='taxon:10118'
FEATURES
source
ORIGIN
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Pred. No.: 0 Length: 7285
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 6 Gaps: 2
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 7286
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 10 Gaps: 2

US-09-611-257A-24 (1-2287) x AF125161 (1-7286)

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Db	478	TGCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTCGATGACTTTCATCTTTGCCTT	537
QY	159	ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCysTy	179
Db	538	CTTTGCTGTGGAATGGTGGTGAAGATGGTGGCCCTTGGGCATCTTTGGGAAGAAATGTTA	597
QY	179	rLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTy	199
Db	598	CCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTTCATTGCAGGGATGCTGGAGTA	657
QY	199	rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr	219
Db	658	TTCGCTGACCTGCAGAACGTACGTTCTCCGCAGTCAGACAGTCCGTGTGTGCGACC	717
QY	219	oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh	239
Db	718	GCTCAGGGCCATTAAACGGGTGCCAGCATGGCATTCGTGCACATTACTGTGTGGACAC	777
QY	239	rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyI1	259
Db	778	CTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTCGTCTTTTTCATCTTTGGCAT	837
QY	259	eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh	279
Db	838	CGTGGCGCTCCAGCTGTGGCAGGACTGCTTCGCAACCGATGCTTCCTCCCCGAGAACTT	897
QY	279	eSerLeuProLeuSerValAspLeuGluProTyrrTyrrGlnThrGluAsnGluAspGluSe	299

Db	898	CAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAAATGAGGACGAGAG	957
QY	299	rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh	319
Db	958	CCCCCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATAGATCCTGCAGGAGTGTGCCAC	1017
QY	319	rLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrrGluThrTyrrAsnSe	339
Db	1018	ACTGCTGGGGAAGCGGTGGTGGCCCCACCCCTGCAGTCTGGACTATGAGACCTATAACAG	1077
QY	339	rSerSerAsnThrThrCysValAsnTrpAsnGlnTyrrTyrrThrAsnCysSerAlaGlyGl	359
Db	1078	TTCCAGCAACACCACTGTGTCAACTGGAACCACTACTATACCAACTGCTCTGCGGGCGA	1137
QY	359	uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrrAlaTrpIleAlaI1	379
Db	1138	GCACAACCCCTTCAAAGGCGCATCAACTTTGACAACTTGGCTATGCCTGGATCGCCAT	1197
QY	379	ePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrrPheValMetAspAlaHi	399
Db	1198	CTTCCAGGTCATCACACTGAGGGCTGGTGCACATCATGTACTTCGTAATGAGCGCTCA	1257
QY	399	sSerPheTyrrAsnPheIleTyrrPheIleLeuLeuIleValGlySerPhePheMetI1	419
Db	1258	CFCCCTTCTACAACTTCATCTACTTCTTCTCATCATCGTGGCTCCTTCTTCATGAT	1317
QY	419	eAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGl	439
Db	1318	CAACCTGTGCTGGTGTGATGGCACGCAGTTCTCCGAGACCAACAGCGGAGAGTCA	1377
QY	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
Db	1378	GCTGATCGGGAGCAGCGGTGACGATTCTCTGTCCATGTAGCACCCCTGGCAAGTTCTC	1437
QY	459	rGluProGlySerCysTyrrGluGluLeuLeuLysTyrrLeuValTyrrIleLeuArgLysAl	479
Db	1438	TGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCCTCCGAAAAGC	1497
QY	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499
Db	1498	AGCCCAAGGCTGGCCAGGCTCTTAGGGCTATAGCGTGCAGGCTGGGCTGCTCAGCAG	1557
QY	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519
Db	1558	CCCAGTGGCCCGTAGTGGGAGGAGCCCCAGCCAGTGGCAGCTGCACCTCGCTCACACCG	1617
QY	519	gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisLe	539
Db	1618	TCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAACCATCACCACTACCACT	1677
QY	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559
Db	1678	GGGTAAATGGGACGCTCAGAGTTCCTCCGGGCCAGCCAGAGATCCAGGACAGGATGCCAA	1737
QY	559	nGlySerArgArgLeuMetLeuProProProProSerThrProThrProSerGlyGlyProPr	579
Db	1738	TGGGTCTCGCCGGCTCATGCTACCAACCCCTCTACACCCACTCCCTCTGGGGGCCCTCC	1797
QY	579	oArgGlyAlaGluSerValHisSerPheTyrrHisAlaAspCysHisLeuGluProValAr	599
Db	1798	GAGGGTGGGAGTCTGTACACAGCTTCTACCATGTGTGACTGCCACTTGGAGCCAGTCCG	1857
QY	599	gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGl	619
Db	1858	TTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGG	1917
QY	619	yLysValTyrrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639
Db	1918	GAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACAGAGATACTGAAGGATAAAGCACT	1977
QY	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGl	659

Db 1978 AGTGGAGGTGGCCCCAGCCCTGGGCCCCCACCCTCACCAGCTTCAACATCCCACCTGG 2037

Qy 659 yPropheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe 679

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Qy 739 pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle 759

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Db 2518 CGCCTTGGAGATGCTGTGAAACTGCTTGCTACGGTCCCTTTGGCTACATTAAGAAATCC 2577

Qy 839 oTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGl 859

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Qy 1156 rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGl 1176

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Qy 2285 pPro 2286

Db 7018 CCCC 7021

RESULT 6

BD224078

LOCUS BD224078 7129 bp DNA linear PAT 17-JUL-2003

DEFINITION T-type calcium channel.

ACCESSION BD224078

VERSION BD224078.1 GI:33033848

KEYWORDS JP 2002525077-A/1.

SOURCE Rattus sp.

ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 7129)

AUTHORS Li,M.

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COMMENT SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION

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PC C12N15/09,A61K31/711,A61K45/00,A61K48/00,A61P3/10,C07K14/47,

PC C07K16/18,

PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/68,G01N33/

PC 15,G01N33/50,

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C12P21/08,

PC C12N15/00,C12N5/00

CC T-type calcium channel

FT key Location/Qualifiers

FT source 1. 7129 /organism='Rattus sp. (rat)'.

FEATURES

source

1. 7129 Location/Qualifiers

/organism="Rattus sp."

/mol_type="genomic DNA"

/db_xref="taxon:10118"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 7129

Score: 11673.00 Matches: 2237

Percent Similarity: 97.77% Conservative: 1

Best Local Similarity: 97.73% Mismatches: 15

Query Match: 97.05% Indels: 36

DB: 6 Gaps: 2

US-09-611-257A-24 (1-2287) x BD224078 (1-7129)

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Db 2 TGGACGAGGAGGAGGATGGAGCGGGCCCGGAGGAGTCGGGACAGCCCCGTAGCTTACGC 61

Qy 54 SerSerThrThrCysProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73

Db 62 AGCTCAACGACCTGTCCGGGGCCGGGGCCCGGAGGGCCGCGGTTCGACGGAAGGACC 121

Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93

Db 122 CGGGCAGCGCGACTCCGAGGCGGAGGGCTGCCGTACCCGGCGCTAGCCCCGGTGT 181

Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAACC 241

Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CGTGGTTCGAGCGAGTCAGTATGCTGTGTCTTCTCAACTGTGTGACTCTGGGTATGT 301

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Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173

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Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193

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RESULT 7

MMU012569

LOCUS MMU012569 7625 bp mRNA linear ROD 09-APR-1999

DEFINITION Mus musculus mRNA for voltage-gated calcium channel, alpha-1-G

ACCESSION AJ012569

VERSION AJ012569.1 GI:4584687

KEYWORDS alfa-1-G subunit; voltage-gated calcium channel.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Klugbauer,N., Marais,E., Lacinova,L. and Hofmann,F.
AUTHORS A T-type calcium channel from mouse brain
TITLE Pflugers Arch. 437 (5), 710-715 (1999)

JOURNAL 99189326

MEDLINE 10087148

PUBMED 2 (bases 1 to 7625)

REFERENCE Klugbauer,N.

AUTHORS Direct Submission

TITLE Submitted (03-NOV-1998) Klugbauer N., Institut fuer Pharmakologie

JOURNAL und Toxikologie, Technische Universitaet Muenchen, Biedersteiner

Str. 29, 80802 Muenchen, GERMANY

FEATURES Location/Qualifiers

source 1. .7625

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US-09-611-257A-24 (1-2287) x MMU012569 (1-7625)

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COMMENT			

Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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/note="ion trans; Region: Ion transport protein. This family contains Sodium, Potassium, Calcium ion channels. This family is 6 transmembrane helices in which the last two helices flank a loop which determines ion selectivity. In some sub-families (e.g. Na channels) the domain is repeated four times, whereas in others (e.g. K channels) the protein forms as a tetramer in the membrane. A bacterial structure of the protein is known for the last two helices but is not the Pfam family due to it lacking the first four helices"
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5227. .5853
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/note="ion trans; Region: Ion transport protein. This family contains Sodium, Potassium, Calcium ion channels. This family is 6 transmembrane helices in which the last two helices flank a loop which determines ion selectivity. In some sub-families (e.g. Na channels) the domain is repeated four times, whereas in others (e.g. K channels) the protein forms as a tetramer in the membrane. A bacterial structure of the protein is known for the last two helices but is not the Pfam family due to it lacking the first four helices"
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ORIGIN
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Alignment Scores:
Pred. No.: 0 Length: 7527
Score: 11489.00 Matches: 2211
Percent Similarity: 96.66% Conservative: 14

Best Local Similarity: 96.05% Mismatches: 43
Query Match: 95.52% Indels: 35
DB: 10 Gaps: 4

US-09-611-257A-24 (1-2287) x BC057399 (1-7527)

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Qy	40	luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProG	60
Db	441	AGCGGGCGCGAGGATCGGGACAGCCCCGGAGCTTCAGCAGCTCAACGACCTGTCTGG	500
Qy	60	lyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGl	79
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Qy	99	pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe	119
Db	621	CAGCCGCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAACCCGTGTTTCGAGCGAGTCAG	680
Qy	119	rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIl	139
Db	681	CATGCTGGTTATTCTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCCGTGTGAGGACAT	740
Qy	139	eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPh	159
Db	741	TGCCCTGTGACTCCCAACGCTGCCGGATCCTGCAGGCCCTTCGACGACTTCACTTTGCCTT	800
Qy	159	ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy	179
Db	801	CTTTGCTGTGGAATGGTGTGAAGATGGTGCCTTTGGGTATCTTTTGGGAAGAAATGTA	860
Qy	179	rLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTy	199
Db	861	CCTGGGAGACACTTGGAACCGGCTTGACTTTTATTCTCTCATTTGCTGGGATGCTGGAGTA	920
Qy	199	rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr	219
Db	921	CTCGCTGGACCTGCAGAAATGTACGTTCTCCGAGTCAGGACAGTCCGTGTGCTGGACC	980
Qy	219	oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh	239
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Qy	239	rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIl	259
Db	1041	CTTGCCCTATGCTGGGCAATGCTCTGCTGCTCTGTTTCTTCGTCTTTTTCATCTTTGGCAT	1100
Qy	259	eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh	279
Db	1101	CGTTGGTGTTCAGCTGTGGGCGGGCTACTTCGAAACCGATGCTTCCTCCCTGAGAAATTT	1160
Qy	279	eSerLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSe	299
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Qy	299	rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh	319
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Qy	319	rLeuArgGlyGluGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSe	339
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Qy	359	uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIl	379
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Qy	379	ePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHi	399
Db	1461	CTTCCAGGTCATCACACTGGAGGGCTGGTGCACATCATGTACTTTTGTGATGGATGCTCA	1520
Qy	399	sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIl	419
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Qy	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
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Qy	459	rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl	479
Db	1650	TGAGCCAGGCAGCTGCTATGAGGAGCTTCTCAAGTACCTGGTGTACATCTCCGCAAAAGC	1709
Qy	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499
Db	1710	AGCCGCGAGGCTGGCCAGGCTCTTAGGGCTGTAGGCGTGGGGTGGGTGTGCTCAGCAG	1769
Qy	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519
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Qy	519	gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisLe	539
Db	1830	TCGTCTGTCTGCCACACCTGGTCCACCACCATCACCCACCATCACCCACTACCACCT	1889
Qy	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559
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Qy	559	nGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGlyProPr	579
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Qy	579	oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr	599
Db	2010	GAGGGTGGGAGTCTGTACACAGCTTCTACCATGTGTGACTGCCACTTGGAGCAGTCCG	2069
Qy	599	gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGl	619
Db	2070	TTGCCAGGCGCCCCCTCCAGGTCCCCATCGGAGGCATCTGGCAGGACTGTGGGTAGTGG	2129
Qy	619	yLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639
Db	2130	GAAGTATACCCCACTGTGCATACCGCCCTCCACAGAGATGTGAAGGATAAGGCACCT	2189
Qy	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGl	659
Db	2190	AGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACAGCTTCAACATCCCACTGG	2249
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Qy 1579 g-----SerLysGluLysGlnMetAlaGluAl 1588

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Qy 1947 gLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGl 1967

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Db 564 TGGAGATGGTGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAAAAGTGTACCTGGGAG 623

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QY 222 laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM 242

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RESULT 10

AF190860 7349 bp mRNA linear PRI 23-FEB-2000

LOCUS

DEFINITION Homo sapiens low voltage-activated T-type calcium channel alpha 1G

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	splice variant CavT.1a (CACNA1G) mRNA, complete cds.	
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	Homo sapiens (human)	
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	Cribbs,L.L., Gomora,J.C., Daud,A.N., Lee,J.H. and Perez-Reyes,E.	
JOURNAL MEDLINE PUBMED	Molecular cloning and functional expression of Ca(v)3.1c, a T-type calcium channel from human brain	
	FEBS Lett. 466 (1), 54-58 (2000)	
	20115462	
	10648811	
REFERENCE AUTHORS TITLE JOURNAL	2 (bases 1 to 7349)	
	Cribbs,L.L., Gomora,J.C., Lee,J.-H., Daud,A.N. and Perez-Reyes,E.	
	Direct Submission	
	Submitted (29-SEP-1999) Physiology, Loyola University Medical Center, 2160 South First Avenue, Maywood, IL 60153, USA	
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ORIGIN	
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ACCESSION AR201015
VERSION AR201015.1 GI:20251903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 7741)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
TITLE DNA encoding human alpha1G-C T-type calcium channel
JOURNAL Patent: US 6358706-A 4 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..7741
/organism="unknown"
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ORIGIN

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Best Local Similarity: 92.38% Mismatches: 112
Query Match: 92.01% Indels: 31
DB: 6 Gaps: 5

US-09-611-257A-24 (1-2287) x AR201015 (1-7741)

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QY 1079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProPros 1099
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QY 1139 rgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG 1159
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Qy 1999 hrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaP 2019
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RESULT 13

AR201014 LOCUS 6822 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 3 from patent US 6358706.

ACCESSION AR201014

VERSION AR201014.1 GI:20251902

KEYWORDS Unknown.

SOURCE

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
TITLE DNA encoding human alphaIG-C T-Type calcium channel
JOURNAL Patent: US 6358706-A.3 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..6822
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
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Score: 10948.50 Matches: 2111
Percent Similarity: 94.03% Conservative: 32
Best Local Similarity: 92.63% Mismatches: 105
Query Match: 91.03% Indels: 31
DB: 6 Gaps: 5

US-09-611-257A-24 (1-2287) x AR201014 (1-6822)

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QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73
Db 62 GGCTCAACGACCTGTCCGGGGCGGGGGCCGGCCGGGGCGGGGTCCAGCAAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCGGTGGTTT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCCTTACTTGAGCCAGGACAGCGCGCCGCGGAGTGGTGTCTCCGCACGGTCTGTAACC 241
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Db 362 ATGACTTCATCTTTGCCCTTCTTGCCGTGGAGATGGTGAAGATGGTGCCCTTGGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
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Qy 1970 laGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleL 1990

Db 5867 CCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCT 5926

Qy 1990 euSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValH 2010

Db 5927 TGTCCGTTCACTCCCGAGCCAGCAGATACCAGCTACATCCTGCAGCTTCCCAAAGATGCAC 5986

Qy 2010 isTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProp 2030

Db 5987 CTCATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCAC 6046

Qy 2030 roGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsps 2050

Db 6047 CAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCAGGCAGCAATAAGGACTGACT 6106

Qy 2050 erLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPros 2070

Db 6107 CCTTGGACGTTTCAAGGTCTGGCAGCCCGGGAAGACCTCTGGCAGAGGTAGTGGGCCCT 6166

Qy 2070 erCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnA 2090

Db 6167 CCCCGCCCTTGGCCCGGGCCCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGC 6226

Db 182 TCCTTACTTGAGCCAGACAGCGCCCGGAGCTGGTGTCTCCGCACGGTCTGTAACC 241
QY 113 roTrrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTGAGCGCATCAGCATGTTGGTCATCCTTCTCAACTGCGTGACCTGGGCATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGGTGCCGATCCTGCGAGGCCTTTG 361
QY 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTTGGCCTTCTTGGCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGTGTCAGGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTGTGCTGGATACGCTGCCCATGCTGGGCAACGTCCTGTGCTGTCTTCTTCTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAACCGAT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCCTTCCTACCTGAGAAATTCAGCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGCGATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAACGTCGCCACGCTGCGGGGACGCGGGGCGGTGGCCCCACCTTGGCGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCCCTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGGAGCAACACCCCTTCAAGGGGCGCCATCAACTTTGACAACTTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCCCTGGATCGCCATCTTCCAGGTTCATCAGCTGGAGGGCTGGGTCCGACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV 413
Db 1082 ACTTTGTGATGGATGCTCATTCCTTCTACAATTTTCATCTACTTTCATCTCCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTCTTCATGATCAACCTGTGCTGGTGGTGTGATGGCCAGCAGTTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGGTGTGCGGTTCCTGTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473

Db 1262 GCACCCCTGGCTAGCTTCTCTGAGCCCCGGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTTTCGTAAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaAlaArgSerGlyGlnGluProGlnProSerGlys 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCCAACCGCGCCTATCCCTCCACACCTGGTGACACCAACCAACCA 1501
QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGGCGAGCCCGGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGGATGCCAATGGGTCCCGCGGTCATGCTGCCACCACTCGACGCCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTGTGTGCACAGCTTCTACCATGCGGACT 1681
QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCCCATCTGAGGCATCCG 1741
QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GQAGGACTGTGGGCAGCGGGAAGGTGTATCCCAACGTCACACCAAGCCCTCCACCGGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
Db 1802 CGCTGAAGGAGAGAGGACTAGTAGAGGTGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCCAACCGGGCCCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGTCTGAAAGCAGACAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGTGTTCCAGACAGCTGCCCTTACTGTGCCCCGGGCGGGGAGGTGGAGCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAAATGCCCTGACTCAGACAGCGAGGAGTATTATGATTTACACAGGATGCCC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCGACCTCCGGGACCCCAACAGC---CGSGGGCAACGGAGCCTGGGCCCAGATG 2158
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAGCTCTGTGCTGGCCTTCTGGAGGCTTAATCTGTGACACCTTCCGAAAGATTG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTTGGCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCA 2278
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACAGCAGCCCGGAGGAGCTTACCAACGCCCTTAGAAATCAGCAACA 2338
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTCACCAGCCTCTTTGGCCTTGAGATGCTGCTGAAGCTGCTTGTGTATGTTCCCT 2398

QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValT	853
DB	2399	TTGGCTACATCAAGATCCCTACAACATCTTCGATGGTGTCTATTGTGGTCATCAGCGTGT	2458
QY	853	rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
DB	2459	GGGAGATCGTGGGCCAGCAGGGGGGGCGCCTGTCCGTGCTGCGGACCTTCCGCCTGATGC	2518
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
DB	2519	GTGTGCTGAAGCTGGTGGCTTCTCGCGCGCTGCAGCGGCAGCTGGTGGTGTCTCATGA	2578
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
DB	2579	AGACCATGGACAACGTGGCCACCTTCTGCATGCTGTATGCTCTTTCATCTTCATCTTCA	2638
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
DB	2639	GCATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGGCTCTGAGCGGGATGGGACACCC	2698
QY	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
DB	2699	TGCCAGACCGGAAGATTTTGACTCTCTTGCTCTGGGCCATCGTCACTGTCTTTCAGATCC	2758
QY	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
DB	2759	TGACCCAGGAGGACTGGAAACAAAGTCTCTACAAATGGTATGGCTCCACGTCGCTCTGGG	2818
QY	973	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993
DB	2819	CGGCCCTTTATTTCAITGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGCTGG	2878
QY	993	alAlaIleLeuValGluGlyPheGlnAlaGlu-----	1003
DB	2879	TCGCCATTCTGGTGGAGGGCTTCAGGGCGGAGGAATCAGCAAACGGGAAGATCGGAGTG	2938
QY	1004	-----GlyAspAlaThrLysSerG	1010
DB	2939	GACAGTTAAGCTGATTACAGCTGCCTGTTCGACTCCAGGGGGGAGATGCCAACAAAGTCCG	2998
QY	1010	luSerGluProAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgL	1030
DB	2999	AATCAGAGCCCGATTCTCTCACCCAGCCTGGATGGTATGGGACAGGAAGAAGTGCT	3058
QY	1030	euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuI	1050
DB	3059	TGGCCTTGGTGTCCCTGGGAGAGACCCCGAGCTCGGAAGAGCCTGCTGCCGCTCTCA	3118
QY	1050	leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG	1070
DB	3119	TCATCCACACGGCCGCACACCCATGTCTGCTGCCCAAGAGCACACGACCGGGCTGGCGG	3178
QY	1070	luAlaLeuGlySerGlySerArgArgThrSerSerGlySerAlaGluProGlyAlaA	1090
DB	3179	AGGCGCTGGGCCCTCGCTCGCGCCGACACCGAGCAGCGGGTTCGGACAGCCTGGGGCGG	3238
QY	1090	laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA	1110
DB	3239	CC---CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTCTCCGCACAGCCCTGGAGCG	3295
QY	1110	laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL	1130
DB	3296	CTGCAAGCAGCTGGACACGAGCGGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCC	3355
QY	1130	euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluS	1150
DB	3356	TGAAGCGGAGAGCCCAAGTGGAGAGCGGGCGGTCTCTGTTGTCGGGAGAGGCCCAGGAGA	3415
QY	1150	erGlnAspGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA	1170
DB	3416	GCCAGGATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGGGGCGATGACCATC	3475

QY	1170	rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG	1190
DB	3476	GCCACAGGGGTCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGC	3535
QY	1190	lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC	1210
DB	3536	AGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACGAGACT	3595
QY	1210	ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL	1230
DB	3596	GCAATGGCAAGTCGGCTTCAGGGCGCTCGCCCGGGCCCTGCGGGCCCTGATGACCCCCAC	3655
QY	1230	euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT	1250
DB	3656	TGGATGGGGATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGCGCGT	3715
QY	1250	rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP	1270
DB	3716	GGATCCGAGCCCGACTCCCTGCCTGCCTCGAGCGAGACTCCTGGTGCAGCCTACATCT	3775
QY	1270	heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA	1290
DB	3776	TCCCTCCTCAGTCCAGGTTCCGCCTCCTGTGTACCGGATCATCACCCACAAGATGTTCTG	3835
QY	1290	spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL	1310
DB	3836	ACCACGTGGTCTTGTATCATCTTCTTAACCTGCATCACCATCGCCATGGAGCGCCCCA	3895
QY	1310	ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA	1330
DB	3896	AAATTGACCCCCACAGCGCTGAACGCATCTTCTTGACCCCTCTCCAATTACATCTTCACCG	3955
QY	1330	laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluG	1350
DB	3956	CAGTCTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACCTGGGCTGGTGTCTCGGGGAGC	4015
QY	1350	lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI	1370
DB	4016	AGCGGTACCTGCGGAGCAGTTGGAACGTGTGGACGGGTGTGGTGTCTCATCTCCGTCA	4075
QY	1370	leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV	1390
DB	4076	TCGACATTTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTTGGGCATGCTGAGGG	4135
QY	1390	alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL	1410
DB	4136	TGCTGCGGCTGCTGCGGACCTTGCGCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGA	4195
QY	1410	ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC	1430
DB	4196	AGCTGGTGGTGGAGACGCTGATGTCTCTCACTGAAACCCCATCGGCAACATTTAGTCTATCT	4255
QY	1430	ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP	1450
DB	4256	GCTGTGCCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTT	4315
QY	1450	heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS	1470
DB	4316	TCGTGTGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCA	4375
QY	1470	erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL	1490
DB	4376	GTTACCGGTGGGTCCGGCACAAAGTACAACCTTGGCCACGCGCCCTGATGTCCC	4435
QY	1490	eupHeValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV	1510
DB	4436	TGTTCTGTTTGGCCCTCCAAGGATGGTTGGTGGACATCATGTACGATGGGCTGGATGCTG	4495
QY	1510	alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS	1530
DB	4496	TGGGCGGTGGACAGCAGCCCATCATGAACCAACCCCTGGATGCTGTGTACTTCTATCT	4555
QY	1530	erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA	1550

Db 4556 CGTTCCTGCTCATGTGGCCCTTCTTGTCTGAACATGTTTGTGGGTGTGGTGGAGA 4615
Qy 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAalaArgArgGluGluLysA 1570
Db 4616 ACTTCCACAAGTGTGGCAGACACAGGAGGAAGAGAGGCCCGCGCGGGAGGAGAAGC 4675
Qy 1570 rgLeuArgArgLeuGluLysLysArgSerLysGluLysGlnMetAlaGluAlaGlnC 1590
Db 4676 GCCTACGAAGACTGGAGAAAAGAGAAAGGAGTAAGGAAAGCAGATGGCTGAAGCCCCAGT 4735
Qy 1590 ysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLysCysThrS 1610
Db 4736 GCAAAACCTTACTACCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACTGTGCACCA 4795
Qy 1610 erHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaM 1630
Db 4796 GCCACTACTGGACCTCTTCATCACAGGTGTCTATCGSGCTGAACGTGGTCAACATGGCCA 4855
Qy 1630 etGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIleP 1650
Db 4856 TGGAGCACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCT 4915
Qy 1650 heThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgP 1670
Db 4916 TCACTGTTCATCTTTGTCTTGGAGTCAGTTTTCAAAACCTGTGGCCCTTTGGTTTCCGTCCGT 4975
Qy 1670 hePheGlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyI 1690
Db 4976 TCTTCCAGACAGGTGGAACCAAGCTGGACCTGGCCATTGTGCTGCTGCCATCATGGGCA 5035
Qy 1690 leThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgI 1710
Db 5036 TCACGCTGGAGGAAATCGAGGTCAACGCCTCGCTGCCCATCAACCCCAACCATCCGCA 5095
Qy 1710 leMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetA 1730
Db 5096 TCATGAGGTGCTGCGCATTTGCCGAGTGCTGAAGCTGTGAAGATGGCTGTGGGCATGC 5155
Qy 1730 rgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuP 1750
Db 5156 GGGCGTGCTGGACACGGTGATGACAGGCCCTTGCCCCAGTGGGGAACCTGGGACTTCTCT 5215
Qy 1750 heMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluC 1770
Db 5216 TCATGTTGTGTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGT 5275
Qy 1770 ysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyM 1790
Db 5276 GTGACGAGACACACCCCTGTGAGGGCCCTGGCCGTCATGCCACCTTTCGGAACCTTGGCA 5335
Qy 1790 etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTTrpAsnGlyIleMetLysA 1810
Db 5336 TGGCCCTTCTTAACCCCTCTTCCAGTCTCCACAGGTGACAANTGGAATGGCATATGAAGG 5395
Qy 1810 spProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleT 1830
Db 5396 ACACCCCTCCGGGACTGTGACCAGGAGTCCACCTGCTACAACACGGTCACTCGCCTATCT 5455
Qy 1830 yrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValL 1850
Db 5456 ACTTTGTGTCTTCGTGCTGACGGCCAGTTTCGTGCTAGTCAACGTGGTATCGCCGTGC 5515
Qy 1850 euMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaG 1870
Db 5516 TGATGAAGCACCTGGAGGAGAGCAACAAGAGGCCCAAGAGGAGGCCGAGCTAGAGGCTG 5575
Qy 1870 luLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProp 1890
Db 5576 AGCTGGAGCTGGAGATGAAGACCTTCAGCCCCCAGCCCCCACTCGCCACTGGGCAGCCCCCT 5635
Qy 1890 heLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProH 1910

Db 5636 TCCTCTGGCCTGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCTGGGGCTCTGC 5695
Qy 1910 isThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValP 1930
Db 5696 ACCAGCGGCCACGCGAGATCAGCTCCCACTTTTCCCTGGAGCACCCCAAGATGCAGC 5755
Qy 1930 rHisProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerG 1950
Db 5756 CCCACCCACGGAGCTGCCA-----GGACCAGACTTACTGACTGTGCGAAGTCTG 5806
Qy 1950 lyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrA 1970
Db 5807 GGETCAGCCGAACGCACTCTCTGCCCAATGACAGCTACATGTGTCTGGCATGGGAGCACTG 5866
Qy 1970 laGluArgSerLeuGlyHisArgGlyTTrpGlyLeuProLysAlaGlnSerGlySerIleL 1990
Db 5867 CCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCT 5926
Qy 1990 euSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValH 2010
Db 5927 TGTCCGTTCACTCCCAAGCAGCAGATACCACTACATCCTGCAGCTTCCCAAGATGCAC 5986
Qy 2010 isTyrLeuLeuGlnProHisGlyAlaProThrTTrpGlyAlaIleProLysLeuProProp 2030
Db 5987 CTCATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAAAGTGCCTCCAC 6046
Qy 2030 roGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspS 2050
Db 6047 CAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAATAAGGACTGACT 6106
Qy 2050 erLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProS 2070
Db 6107 CCTTGGACGTTCAGGGTCTGGGCAGCCGGGAAGACCTGTGGCAGAGGTAGTGGGCCCT 6166
Qy 2070 erCysProLeuThrArgSerSerSerPheTTrpGlyGlySerSerIleGlnValGlnGlnA 2090
Db 6167 CCGCGCCCTGGCCGGGCTACTCTTTCTGGGGCAGTCAAGTACCCAGGCACAGCAGC 6226
Qy 2090 rgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyL 2110
Db 6227 ACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCCCGCCAGCCCTTGGCCAGGCC 6286
Qy 2110 euGluProSerTTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrG 2130
Db 6287 CAGAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAACGAGCTTAGAGTTGGACACGG 6346
Qy 2130 luLeuSerTTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluGluProLeuPheP 2149
Db 6347 AGCTAGCTGGATTTCAGGAGACCTCCTGCCCCCTGGCGGCCAGGAGAGCCCCCATCCC 6406
Qy 2149 roArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyP 2169
Db 6407 CACGGACCTGAAGAAGTGTACAGCGTGGAGGCCACAGAGCTGCCAGCGCGGCCACACGT 6466
Qy 2169 heTTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerG 2189
Db 6467 CCTGGCTGGATGAGCAGAGAGACACTCTATCGCCCTCAGCTGCCTGGACAGCGGTCCC 6526
Qy 2189 lnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlyS 2209
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Qy 2209 erArgProLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnG 2229
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VERSION AF227746.1 GI:7159264
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6897)
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha(1G) subunit
that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6897)
AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US09611257_QCGN_1_1_863 @runat 26042005_150448 14882 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :		N Geneseq_16Dec04:*	
		1:	Geneseqn1980s:*
		2:	Geneseqn1990s:*
		3:	Geneseqn2000s:*
		4:	Geneseqn2001as:*
		5:	Geneseqn2001bs:*
		6:	Geneseqn2002as:*
		7:	Geneseqn2002bs:*
		8:	Geneseqn2003as:*
		9:	Geneseqn2003bs:*
		10:	Geneseqn2003cs:*
		11:	Geneseqn2003ds:*
		12:	Geneseqn2004as:*
		13:	Geneseqn2004bs:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	12024	100.0 7540 5	AAF31677 Aaf31677 Rat alpha
2	11980	99.6 6942 13	ADSL6295 Adsl6295 Rat volta
3	11829	98.3 7286 3	AAZ52309 Aaz52309 Rat pancr
4	11798	98.1 6762 2	AAx83485 Aax83485 Rat T-typ
5	11767	97.8 6816 2	AAx83487 Aax83487 Rat T-typ

ALIGNMENTS

RESULT 1		AAF31677	
ID	AAF31677	standard; cDNA; 7540 BP.	
XX			
AC	AAF31677;		
XX			
DT	09-APR-2001	(first entry)	
XX			
DE	Rat alpha-IG calcium channel cDNA.		
XX			
KW	Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;		
KW	hypotensive; cardiant; nootropic; T-type calcium channel subunit;		
KW	cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;		
XX			
OS	Rattus sp.		
XX			
PN	WO200102561-A2.		
XX			
PD	11-JAN-2001.		
XX			
PF	04-JUL-2000; 2000WO-CA000794.		
XX			
PR	02-JUL-1999; 99US-00346794.		
XX			
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.		
XX			
PI	Snutch TP, Baillie DL;		
XX			

6	11751.5	97.7	6795	2	AAx83486	Aax83486 Rat T-typ
7	11747.5	97.7	6741	2	AAx83488	Aax83488 Rat T-typ
8	11066.5	92.0	7741	4	AAD04756	Aad04756 Human T-t
9	10970	91.2	6750	2	AAx83481	Aax83481 Human T-t
10	10946	91.0	6804	2	AAx83483	Aax83483 Human T-t
11	10923.5	90.8	6783	2	AAx83482	Aax83482 Human T-t
12	10919.5	90.8	6729	2	AAx83484	Aax83484 Human T-t
13	10916	90.8	6892	5	AAF31684	Aaf31684 Human alp
14	10845.5	90.2	7648	13	ADQ89063	Adq89063 Human uro
15	10845.5	90.2	7648	13	ADSL6298	Adsl6298 Human vol
16	10843.5	90.2	8002	4	AAH98402	Aah98402 Human EST
17	6248	51.9	8447	5	AAF31678	Aaf31678 Rat alpha
18	6243	51.9	7898	2	AAx59081	Aax59081 Human act
19	6242	51.9	7898	8	ABZ58365	Abz58365 Human T-t
20	6241	51.9	7898	2	AAx59080	Aax59080 Human act
21	6103	50.7	3993	4	AAAS01624	Aas01624 Human T-t
22	5895	49.0	6132	2	AAx83489	Aax83489 Human T-t
23	5886	48.9	6114	2	AAx83490	Aax83490 Human T-t
24	5738.5	47.7	6941	2	AAx59082	Aax59082 Human act
25	5432.5	45.2	6990	13	ADSL6296	Adsl6296 Human vol
26	5420	45.1	6816	6	AAAS16826	Aas16826 Human T-t
27	5420	45.1	6816	8	ABX93560	Abx93560 Human CDN
28	5420	45.1	6816	12	ADH69264	Adh69264 Human TCC
29	5420	45.1	6855	6	AAAS16827	Aas16827 Human T-t
30	5420	45.1	6855	8	ABX93561	Abx93561 Human CDN
31	5420	45.1	6855	12	ADH69266	Adh69266 Human TCC
32	5407	45.0	6503	12	ADH69275	Adh69275 Rat TCCV
33	5346.5	44.5	5469	2	AAx83491	Aax83491 Human T-t
34	5345	44.4	5505	2	AAx83492	Aax83492 Rat T-typ
35	5200.5	43.2	5735	5	AAF31679	Aaf31679 Rat brain
36	3950	32.8	5562	2	AAV57542	Aav57542 Human cal
37	3950	32.8	5562	5	AAF31674	Aaf31674 Human alp
38	3937.5	32.7	7969	4	ABL07263	Ab107263 Drosophil
39	3861.5	32.1	6073	13	ADSL6299	Adsl6299 C. elegan
40	3399.5	28.3	6933	5	AAAS75141	Aas75141 DNA encod
41	3356	27.9	2212	5	AAF31681	Aaf31681 Human alp
42	2091.5	17.4	3464	4	AAK94358	Aak94358 Human ful
43	2091.5	17.4	3464	12	ADL31040	Adl31040 Full leng
44	1974	16.4	1669	2	AAx59083	Aax59083 Human act
45	1751.5	14.6	7362	2	AAQ37817	Aaq37817 Sequence

DR WPI; 2001-123111/13.
DR P-PSDB; AAB66475.
XX
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
PS Example 2; Page 61-63; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX
SQ Sequence 7540 BP; 1502 A; 2313 C; 2161 G; 1564 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7540
Score: 12024.00 Matches: 2286
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.97% Indels: 0
DB: 5 Gaps: 0

US-09-611-257A-24 (1-2287) x AAF31677 (1-7540)

QY	1	MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg	20
Db	385	ATGCTCCCCACCGGGTCCCGGTCGCTGAGGACACCTCTCTGAGGGCTCCGCTCGC	444
QY	21	ProSerSerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu	40
Db	445	CCCTCTCGGACCCCCCGGGCCCCGGCTGGCCAGAGGATGGACGAGGAGGATGGAG	504
QY	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGly	60
Db	505	CGGGCGCGAGAGTCCGGGACAGCCCCGCTAGCTTCACGCAGCTCAACGACCTGTCCGGG	564
QY	61	ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla	80
Db	565	CCGGGCGCGCAGGGCCGGGTCGACGGAAGGACCGGGCAGCGCGGACTCCGAGGCG	624
QY	81	GluGlyLeuProTyProAlaLeuAlaProValValPhePheTyLeuSerGlnAspSer	100
Db	625	GAGGGGCTCCGTACCCGGCGTAGCCCCGGTGGTTTCTTCTACTTGAGCCAGGACAGC	684
QY	101	ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet	120
Db	685	CGCCCCGGAGCTGGTGTCTCCGACGGTCTGTAAACCGTGGTTCGAGCGAGTCAGTATG	744
QY	121	LeuValLeuLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAla	140
Db	745	CTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCCGTGTGAGGACATTGCC	804
QY	141	CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePhe	160
Db	805	TGTGACTCCAGCGCTCCGGATCCGAGCTTCGAGGCCCTTCGATGACTTCTATCTTTGCCTCTTT	864
QY	161	AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyLeu	180
Db	865	GCTGTGGAATGGTGGTGAAGATGGTGGCTTGGGCATCTTGGGAAAGAAATGTACCTG	924
QY	181	GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTySer	200
Db	925	GGAGACACTTGAACCGGCTTGACTTTTTCATTGTTCATTGCAGGGATGCTGGAGTATTCG	984
QY	201	LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu	220

Db	985	CTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGGACAGTCCGTGTGCTGCGACCGCTC	1044
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu	240
Db	1045	AGGGCCATTAAACCGGTGCCAGCATGCGCATTTCTCGTCACATTACTGCTGGACACCTTG	1104
QY	241	ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal	260
Db	1105	CCTATGCTGGGCAACGTCCTGCTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1164
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
Db	1165	GGCGTCCAGCTGTGGCAGGACTGCTTCGCAACCGGTGCTTCTCTCCCGAGAACTTCAGC	1224
QY	281	LeuProLeuSerValAspLeuGluProTyTrpGlnThrGluAsnGluAspGluSerPro	300
Db	1225	CTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAATGAGGACGAGAGCCCC	1284
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
Db	1285	TTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGATCCTGCAGGAGTGTGCCACACTG	1344
QY	321	ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyTrpGluThrTyAsnSerSer	340
Db	1345	CGTGGGAAGCGGTGGTGGCCCCACCTGCAGTCTGGACTATGAGACCTATAACAGTTCC	1404
QY	341	SerAsnThrThrCysValAsnTrpAsnGlnTyTrpThrAsnCysSerAlaGlyGluHis	360
Db	1405	AGCAACACCACTGTGTCAACTGGAACCACTACTATACCACTGCTCTCGGGCGGAGCAC	1464
QY	361	AsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyAlaTrpIleAlaIlePhe	380
Db	1465	AAACCCCTTCAAAGCGCCCATCAACTTGACAAACATTGGCTATGCCTGGATCGCCATCTTC	1524
QY	381	GlnValIleThrLeuGluGlyTrpValAspIleMetTyTrpPheValMetAspAlaHisSer	400
Db	1525	CAGGTTCATCACACTGGAGGGCTGGGTGCACATCATGTACTTTCGTAATGGACGCTCCTCC	1584
QY	401	PheTyAsnPheIleTyPheIleLeuLeuIleIleValGlySerPhePheMetIleAsn	420
Db	1585	TTCTACAACTTCATCTACTTCTTCTTCTCATCATCATCGTGGGCTCTTCTTCTCATGATCAAC	1644
QY	421	LeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu	440
Db	1645	CTGTGCCTGGTGGTATTGCCACGCGAGTTCTCCGAGACCAACAGCGGGAGAGTCAGCTG	1704
QY	441	MetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlu	460
Db	1705	ATGCGGGAGCAGCGGTACGATTCTCTGCAATGCTAGCACCTGGCAAGCTTCTCTGAG	1764
QY	461	ProGlySerCysTyTrpGluLeuLeuLysTyTrpValTyIleLeuArgLysAlaAla	480
Db	1765	CCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCTCCGAAAAGCAGCC	1824
QY	481	ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPro	500
Db	1825	CGAAGGCTGGCCAGGTCTCTAGGGCTATAGCGGTGGGGCTGGGCTGCTCAGCAGCCCA	1884
QY	501	ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg	520
Db	1885	GTGGCCCGTAGTGGGCGAGGAGCCCCAGCCAGTGGCAGCTGCATCTCGTCAACCGTCTGT	1944
QY	521	LeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisLeuGly	540
Db	1945	CTGTCTGTCCACCACCTGGTCCACCACCATCACCAACCATCACCACTACCACTGGGT	2004
QY	541	AsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly	560
Db	2005	AATGGACGCTCAGAGTTCCTCCGGGCCAGCCAGAGATCCAGGACAGGATGCCAATGGG	2064
QY	561	SerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg	580
Db	2065	TCTCGCCGGCTCATGTCTACCAACCACTCTACACCACTCTCTCTCTCTCTCTCTCTCTCT	2124

Qy 581 GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCys 600
Db 2125 GGTGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCGTTGC 2184
Qy 601 GlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys 620
Db 2185 CAGGACCCCTCCAGATGCCATCGGAGGCATCTGGTAGGACTGTGGTAGTGGGAAG 2244
Qy 621 ValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuVal 640
Db 2245 GTGTACCCCACTGTGCATACCAGCCCTCCACCAGAGACTGAAGGATAAAGCACTAGTG 2304
Qy 641 GluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyPro 660
Db 2305 GAGGTGGCCCCAGCCCTGGGCCCCCCACCCTCACAGCTTCAACATCCACCTGGGCC 2364
Qy 661 PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys 680
Db 2365 TTCAGTCCATGCACAAGCTCCTGGAGACACAGAGTACGGAGCCTGCCATAGCTCCTGC 2424
Qy 681 LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
Db 2425 AAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCCTGCGGGCCGGACAGTTGTCCC 2484
Qy 701 TyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSer 720
Db 2485 TACTGTCCCCGACAGGAGCAGGAGAGCCAGAGTCCGCTGACCATGTCTATGCCTGACTCA 2544
Qy 721 AspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro 740
Db 2545 GACAGCGAGGCTGTGTATGAGTTACACAGGACGCTCAGACAGTACCTCCGGGATCCC 2604
Qy 741 HisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla 760
Db 2605 CACAGCGGGCGGACAGCGAGCCTGGGCCAGATGCAGAGCCTAGTTCTGTGTGGCT 2664
Qy 761 PheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArg 780
Db 2665 TTCTGGAGGCTGATCTGTGACACATTCGGAAGATCTAGATAGCAAAATACTTTGGCCGG 2724
Qy 781 GlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGln 800
Db 2725 GGAATCATGATCGCCATCCTGGTCAATACACTCAGCATGGGCATCGAGTACCAGGACAG 2784
Qy 801 ProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAla 820
Db 2785 CCCGAGGAGCTCACCAACGCCCTGGAAATCAGAAATCAGAACATCGTCTTACCAGCCTCTTCGCC 2844
Qy 821 LeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyr 840
Db 2845 TTGGAGATGCTGCTGAAACTGCTGTCTACGGTCCCTTTGGCTACATTAAAGAAATCCCTAC 2904
Qy 841 AsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnGly 860
Db 2905 AACATCTTTGATGGTGTCAATTGTGGTCATCAGTGTGTGGGAGATTGTGGGCCAGCAGGGA 2964
Qy 861 GlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe 880
Db 2965 GGTGGCCTGTGGTGTCTCGGACCTTCCGCCCTGATGCGGGTGTGAAGCTGGTGGCCTTC 3024
Qy 881 LeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThr 900
Db 3025 CTGCCGCCCTGCAGCGCCAGCTCGTGGTGTCTCATGAAGACCATGGACAACGTTGGCCACC 3084
Qy 901 PheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPhe 920
Db 3085 TTCTGCATGCTCCTCATGCTGTTCATCTTTCATCTTTCAGCATCCTGGGCATGCATCTCTTT 3144
Qy 921 GlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsp 940
Db 3145 GGTGCAAGTTCCGATCTGAACGGGATGGGGACACGTTGCCAGACCCGGGAAGAATTTCCGAC 3204

Qy 941 SerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLys 960
Db 3205 TCCTGTCTTGGGCCATCGTCACTGTCTTTAGATTCTGACTCAGGAAGACTGGAATAAA 3264
Qy 961 ValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeu 980
Db 3265 GTCTCTACAAACGGCATGGCCTCCACATCGTCTTGGGTGCTCTTTACTTTCATCGCCCTC 3324
Qy 981 MetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPhe 1000
Db 3325 ATGACTTTTGGCAACTATGTCTCTTTAACCTGTGTGGCCATTCTTGTGGAAGGATTTC 3384
Qy 1001 GlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal 1020
Db 3385 CAGGACAGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTCGCCCAGTGTG 3444
Qy 1021 AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
Db 3445 GATGTTGATGGGACAGAAAGAACGCTTGGCCCTGGTGGCTTTGGGAGAACACGCGGAA 3504
Qy 1041 LeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHis 1060
Db 3505 CTACGAAAAGAGCCTTTTGGCACCCCTCATCATCATACGGCTGCGACACCAATGTTCACAC 3564
Qy 1061 ProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSer 1080
Db 3565 CCCAAGAGCTCCAGCACAGGTGTGGGGAAGCACTGGGCTCTGGCTCTCGACGTACCAGT 3624
Qy 1081 SerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAla 1100
Db 3625 AGCAGTGGTCCGCTGAGCCTGGAGCTGCCCAACCATGAGATGAAATGTCCGCCAAGTGCC 3684
Qy 1101 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSer 1120
Db 3685 CGCAGCTCCCCGCACAGTCCCTGGAGTGGCGCAAGCAGCTGGACCAAGCGCGCTCCAGC 3744
Qy 1121 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArg 1140
Db 3745 AGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGGAGGAGCCCCGAGCGGGAGCGGAGG 3804
Qy 1141 SerLeuLeuSerGlyGlyGlyGlnGluSerGlnAspGluGluSerSerGlyGluAsp 1160
Db 3805 TCCTGTCTGTCTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAAGTTCAGAAGAGGAC 3864
Qy 1161 ArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLys 1180
Db 3865 CGGGCCAGCCAGCAGCAGTACCATCGCCACAGGGTTCTCTTGGAACTGTAGGCCCAAG 3924
Qy 1181 SerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGly 1200
Db 3925 AGTTCCTTTGACCTGCTGACACTCTGCAGGTGTCGGGGGTGCACCCGACAGCCAGCGGC 3984
Qy 1201 ArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1220
Db 3985 CGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCC 4044
Qy 1221 ArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsn 1240
Db 4045 CGCACCTCTGAGGACTGATGACCCCCCACTGGATGGGATGATGACAATGATGAGGGAAT 4104
Qy 1241 LeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArg 1260
Db 4105 CTGAGCAAAGGGGAACGCATACAAGCCTGGGTGAGTCCGGCTTCCTGCCTGTGTGCCGA 4164
Qy 1261 GluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCys 1280
Db 4165 GACGAGATTCTCTGGTCGGCCTATATCTTTCTCTCAGTCAAGGTTTCGTCTCTCTGTGT 4224
Qy 1281 HisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsn 1300
Db 4225 CACCGGATCATACCCACAAGATGTTTGACCATGTGGTCTCTCGTCATCATCTTCTCTCAAC 4284
Qy 1301 CysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePhe 1320

||||| 4285 TGTATCACCATCGCTATGGAGCGGCCCAAAATTGACCCCCACAGCGCTGAGCGCATCTTC 4344 Db
||||| 1321 LeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValIysVal 1340 QY
||||| 4345 CTGACCCCTCTCCAACTACATCTTACCGCAGTCTTTCTAGCTGAATGACAGTGAAGGTG 4404 Db
||||| 1341 ValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeu 1360 QY
||||| 4405 GTGGCACTGGGCTGGTCTTTGGGAGCAGGCCTACCTGCGCAGCAGCTGGAATGTGCTG 4464 Db
||||| 1361 AspGlyLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSer 1380 QY
||||| 4465 GACGGCTTGTGTGCTCATCTCCGTCAATCGACATCCTGTGCTCCATGGTCTCCGACAGC 4524 Db
||||| 1381 GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeu 1400 QY
||||| 4525 GGCACCAAGATCCTTGGCATGCTGAGGGTGTGCGGTGCTGCGGACCCCTGCGTCCACTC 4584 Db
||||| 1401 ArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeu 1420 QY
||||| 4585 AGGTCATCAGCCGGGCCAGGGACTGAAGCTGGTGGTAGAGACTCTGATGTATCCCTC 4644 Db
||||| 1421 LysProIleGlyAsnIleValIleCysCysAlaPhePheIlePheGlyIleLeu 1440 QY
||||| 4645 AAACCCATTGGCAACATTGTGGTCAATTGCTGTGCCTTCTTCATCATTTTGGAAATCTC 4704 Db
||||| 1441 GlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnIle 1460 QY
||||| 4705 GGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGTCAGGTCCGGCCTCCAAAGATGGTTGGGTT 4764 Db
||||| 1461 ThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPhe 1480 QY
||||| 4765 ACTAACAAAATCCGACTGCGCTGAGGCCAGCTACCGATGGTCCGGCACAAGTACAACITT 4824 Db
||||| 1481 AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal 1500 QY
||||| 4825 GACAACCTGGGCCAGGCTCTGATGTCCTGTTGTGCTGGCCTCCAAAGATGGTTGGGTT 4884 Db
||||| 1501 AspileMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHis 1520 QY
||||| 4885 GACATCATGTATGATGGCTGGATGCTGTGGGTGTGGATCAGCAGCCCATCATGAACCCAC 4944 Db
||||| 1521 AsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeu 1540 QY
||||| 4945 AACCCCTGGATGCTGCTATACTTCACTCTCCTTCCTCCTCATCGTGGCCTTCTTTGTCTCTG 5004 Db
||||| 1541 AsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGlu 1560 QY
||||| 5005 AACATGTTTGTGGCGTGGTGTGGAGAACTTCCATAAGTGCAGACAGCAGCAGGAGGAG 5064 Db
||||| 1561 GluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSer 1580 QY
||||| 5065 GAGGAGCGGAGCGCGGTGAGGAGAAGCGACTACGGAGGCTGGAGAAAAGAGAGAGGAGT 5124 Db
||||| 1581 LysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1600 QY
||||| 5125 AAGGAGAAGCAGATGGCCGAAGCCAGTGCAAGCCCTACTACTGTACTACTCGAGATTTC 5184 Db
||||| 1601 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1620 QY
||||| 5185 CGGCTCCTTGTCCACCACCTGTGTACAGCCACTACCTGGACCTCTTCATCACTACTGGTGTG 5244 Db
||||| 1621 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1640 QY
||||| 5245 ATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACAGCAGCCCCCAGATCCTGGAC 5304 Db
||||| 1641 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPhe 1660 QY
||||| 5305 GAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTTGTCTTTGTGATCAGTTTTC 5364 Db
||||| 1661 LysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu 1680 QY

5365 AACTTGTGGCCTTTTGGCTTCGCGCTTCTTCCAGGACAGGTGGAAACCAGCTGGACCTG 5424 Db
1681 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSer 1700 QY
||||| 5425 GCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTCTG 5484 Db
1701 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1720 QY
||||| 5485 CTGCCCATCAACCCCATCATCCGTATCATGAGGGTGTCCGCAATTGCTCGAGTTCTG 5544 Db
1721 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeu 1740 QY
||||| 5545 AAGCTGTTGAAGATGGCTGGGCATGCGGCACCTGCTGCACACGGTGTGTCAGGCCCTG 5604 Db
1741 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1760 QY
||||| 5605 CCCCAGGTGGGAACCTGGGACTTCTTTCATGTATTGTTTTTTCATCTTTGCAGCTCTG 5664 Db
1761 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1780 QY
||||| 5665 GCGGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGGGT 5724 Db
1781 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1800 QY
||||| 5725 CGGCATGCCACCTTTAGGAACCTTGGTATGGCTTCTGACCCCTTCTCCGAGTCTCCACT 5784 Db
1801 GlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThr 1820 QY
||||| 5785 GGTGACAACTGGAATGGTATTATGAAGGACCCCTTCCCGGACTGTGACCAGGAGTCCACC 5844 Db
1821 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1840 QY
||||| 5845 TGCTACAACTGTCTCTCCCTTACTACTTGTGTCTCGTCTGACGGCCAGTTT 5904 Db
1841 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1860 QY
||||| 5905 GTGCTGGTCAACGTGGTCAATAGCTGTGTGATGAAGCACTGGAAGAAAGCAACAAGAG 5964 Db
1861 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1880 QY
||||| 5965 GCCAAGGAGGAGCGGAGCTCGAGCGGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCG 6024 Db
1881 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSer 1900 QY
||||| 6025 CAGCCCCACTCCCGCTGGGAGCCCTTCTCTGGCCCGGGGTGGAGGTGTCAACAGT 6084 Db
1901 ThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGly 1920 QY
||||| 6085 ACTGACAGCCCTAAGCCTGGGGCTCCACACCACTGCCCAATGGAGCAGCCTCGGGC 6144 Db
1921 PheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGly 1940 QY
||||| 6145 TTCTCCCTTGAGCACCCACGATGGTACCCACCCAGGAGGTGCCAGTCTTGTCCCAATGAC 6204 Db
1941 ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAsp 1960 QY
||||| 6205 CCAGACCTGTGCTGCTGAGGAAGTCTGTGTCTGAGGATCCCTAGGACGCACTCTGTGCCAATGAC 6264 Db
1961 SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGly 1980 QY
||||| 6265 AGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGCGGTGGGG 6324 Db
1981 LeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSer 2000 QY
||||| 6325 CTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCCTCCCAACCAGCAGACACCAGC 6384 Db
2001 CysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThr 2020 QY
||||| 6385 TGCATCCTACAGCTTCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGGTCCCACC 6444 Db
2021 TrpGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeu 2040 QY
||||| 6445 TGGGGCGCCATCCCTAAACTACCCCACTGGCGCTCCCTCTCTGGCTCAGAGGCTCTC 6504 Db

QY 2041 ArgArgGlnAlaAlaileArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu 2060
|
Db 6505 AGCGCCAGGAGCAATAAGGACTGACTCCCTGGATGTGAGGGCCTGGGTAGCCGGAA 6564

QY 2061 AspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrp 2080
|
Db 6565 GACCTGTGTGAGAGGTGAGTGGGCCCTCTGCCCCCTGACCCCGTCTCATCTTCTGG 6624

QY 2081 GlyGlySerSerIleGlnValGlnArgSerGlyIleGlnSerLysValSerLysHis 2100
|
Db 6625 GCGGGTTCGAGCATCCAGGTGCAGAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAGCAC 6684

QY 2101 IleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProGlu 2120
|
Db 6685 ATCCGCTGCCAGCCCTTGCCAGGCTTGGAAACCCAGCTGGGCCAAGGACCTCCAGAG 6744

QY 2121 ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuPro 2140
|
Db 6745 ACCAGAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTTCCC 6804

QY 2141 SerSerGlnGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThr 2160
|
Db 6805 AGCAGCCAGGAAGAACCCCTGTTCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACC 6864

QY 2161 GlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAla 2180
|
Db 6865 CAGAGCTGCAGGCGCAGGCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTGCT 6924

QY 2181 ValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGly 2200
|
Db 6925 GTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCGGG 6984

QY 2201 GlyGlnProGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2220
|
Db 6985 GGCCAACTCTTGGGGTCTCTGGAGCCGGCCTAAGAAAAAACTCAGCCCCCAGTATC 7044

QY 2221 SerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeu 2240
|
Db 7045 TCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCTGTGTCTGCCTC 7104

QY 2241 ArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSer 2260
|
Db 7105 AGGAGGAGGCGCGCCAGTACTTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGC 7164

QY 2261 ThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAsp 2280
|
Db 7165 ACGGTGCTCCTACCCCTCCCAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGAC 7224

QY 2281 ProThrAspMetAspPro 2286
|
Db 7225 CCAACAGACATGGACCCC 7242

RESULT 2

ADSL6295
ID ADSL6295 standard; DNA; 6942 BP.
XX
AC ADSL6295;
XX
DT 02-DEC-2004 (first entry)
XX
DE Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.
XX Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.
XX
OS Rattus norvegicus.
XX
PN US2004175761-A1.
XX
PD 09-SEP-2004.
XX

PF 01-MAR-2003; 2003US-00377139.
XX
PR 01-MAR-2003; 2003US-00377139.
XX
PA (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX

PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX
XX WPI; 2004-642122/62.
DR REFSEQ; NM_031601.
XX

PT Screening drug candidates that target voltage dependent ion channel
PT protein, involves contacting screening protein with chemical compound,
PT which is drug candidate and determining whether chemical compound binds
PT to screening protein.
XX

PS Disclosure; SEQ ID NO 7; 61pp; English.
XX

CC The invention relates to the composition of matter suitable for use in
CC identifying chemical compounds that bind to voltage-dependent ion channel
CC proteins. The composition comprises a screening protein that consists of
CC an ion channel voltage sensor domain of the ion channel protein
CC immobilised on a solid support. The invention is useful for identifying
CC chemical compounds (drug candidate) that bind to voltage-dependent ion
CC channel proteins. The drug candidate of the invention is utilised for
CC treating a condition mediated by aberrant electrical activity that
CC initiates uptake or release of neurotransmitters and contraction of
CC muscles. The drug candidate of the invention is also utilised for
CC treating epilepsy and arrhythmia. The present sequence is a voltage-
CC dependent calcium channel DNA.
XX

SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6942
Score: 11980.00 Matches: 2283
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 3
Query Match: 99.60% Indels: 2
DB: 13 Gaps: 0

US-09-611-257A-24 (1-2287) x ADSL6295 (1-6942)

QY 1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20
|
Db 16 ATGCTCCCCACCGGGTCCCCGTTGGTGAGGACACCTCCTCTGAGGGGCTCGCTCGC 75

QY 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
|
Db 76 CCTCTTCGGACCCCCCGGGCCCCGGCTGGCCAGAGGATGGACGAGGAGGATGGAG 135

QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
|
Db 136 CCGGCGCCGAGGAGTCCGGACAGCCCCCGTAGCTTCACGCAGCTCAACGACCTGTCGCGG 195

QY 61 ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluA 80
|
Db 196 CCGGGGCGCGCAGGGCGCGGGTCCGACGAAAGAACCCCGGCAGCGCGGACTCCGAGG 255

QY 80 laGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspS 100
|
Db 256 CGAGGGGCTGCCGTACCCCGCGCTAGCCCCGGTGGTTTCTTCTACTTGAGCCAGGACA 315

QY 100 erArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerM 120
|
Db 316 GCCGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAACCCCGTGGTTCGAGCGAGTCAGTA 375

QY 120 etLeuValIleLeuLeuAenCysValThrLeuGlyMetPheArgProCysGluAspIleA 140
|
Db 376 TGCTGGTCAATCTTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCCGTTGTGAGGACATTG 435

QY	140	laCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPheP	160	roValAlaAArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA	520	
Db	436	CCTGTGACTCCAGCGCTCCGGATCCCTGCAGGCCCTTCGATGACTTCATCTTTGCCCTTCT	495	1516	CAGTGGCCCGTAGTGGCAGAGAGCCCGAGCCAGTGGCAGCTGCACTCGCTCACACCGTC	1575
QY	160	heAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrL	180	520	rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisLeuG	540
Db	496	TTGCTGTGGAATGGTGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAGAAATGTTACC	555	1576	GTCTGTCTGTCCACCACCTGGTCCACCACCACCATCACACCACCATCACCACTACCACTGG	1635
QY	180	euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS	200	540	lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG	560
Db	556	TGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTTGTCAATTCAGGGATGCTGGAGTATT	615	1636	GTAAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGGACAGGGATGCCAATG	1695
QY	200	erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL	220	560	lySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA	580
Db	616	CGCTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGGACAGTCCGTGTGTGCGACCGC	675	1696	GGTCTCGCCGGCTCATGTACACAGCTTCTACCATCCACCACTTACACCACTCCCTCTGGGGGCCCTCCGA	1755
QY	220	euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL	240	580	rgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC	600
Db	676	TCAGGGCCATTAAACCGGTGCCAGCATGCGCATTCCTCGTCACATTACTGCTGGACACCT	735	1756	GGGTGGCGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTTGGAGCCAGTCCGTT	1815
QY	240	euProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleV	260	600	ysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL	620
Db	736	TGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTCTGTTTCTTCTTCTTCTG	795	1816	GCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGGGA	1875
QY	260	alGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheS	280	620	ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV	640
Db	796	TGGGCGTCCAGCTGTGGCAGGACTGCTTCGCAACCGGTGCTTCCTCCCGGAGAACTTCA	855	1876	AGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAGAGATACTGAAGGATAAAGCACTAG	1935
QY	280	erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP	300	640	alGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyP	660
Db	856	GCCTCCCGCTGAGCGTGGACCTGGAGCCTTATTACCAGACAGAGAAATGAGACGAGGCC	915	1936	TGGAGTGGCCCCCAGCCCTGGGCCCCCCCCACCCCTCACAGCTTCAACATCCACACTGGGC	1995
QY	300	roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL	320	660	roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC	680
Db	916	CCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGATCCTGCAGGAGTGTGCCACAC	975	1996	CCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTACGGGAGCCTGCCATAGTCTCT	2055
QY	320	euArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS	340	680	ysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP	700
Db	976	TGCGTGGGAAGGCGGTGGTGGCCACCCCTGCAGTCTGGACTATGAGACCTATAACAGTT	1035	2056	GCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCCTCGGGCCGGACAGTTGTC	2115
QY	340	erSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH	360	700	roTyrCysAlaAArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAsps	720
Db	1036	CCAGCAACACCACTGTGTCAACTGGAACCACTACTATACCAACTGCTCTCGGGCGGAGC	1095	2116	CCTACTGTGCCCGACAGGAGCAGGAGAGCCAGAGTCCGCTGACCATGTATGCCTGACT	2175
QY	360	isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP	380	720	erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspp	740
Db	1096	ACAACCCCTTCAAAGCGCCATCAACTTTGACAACAATTGGCTATGCCTGGATCGCCATCT	1155	2176	CAGACAGCGAGCGTGTATGATGATTCACACAGGACGCTCAGCACAGTGACCTCCGGGATC	2235
QY	380	heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisS	400	740	roHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA	760
Db	1156	TCCAGGTATACACTGGAGGGCTGGGTGCGACATCATGTACTTCGTAATGGACGCTCACT	1215	2236	CCCACAGCCGGCGGACAGCGGAGCCTGGGCCCCAGATGCAGAGCCCTAGTTCTGTGCTGG	2295
QY	400	erPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleA	420	760	laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA	780
Db	1216	CCTTCTAACAATTCATCTACTTCTCATCATCGTGGGCTCCTTCTTCTATGATCA	1275	2296	CTTCTGGAGGCTGATCTGTGACACATTCGGAAGATCGTAGATAGCAATACTTTGGCC	2355
QY	420	snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL	440	780	rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG	800
Db	1276	ACCTGTGCCTGGTGGTATTGCCACGCGAGTTCTCCGAGACCAACAGCGGGAGAGTCAGC	1335	2356	GGGAATCATGATCGCCATCTCTGGTCAATACTCAGCATGGGCATCGAGTACCAGCAGC	2415
QY	440	euMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG	460	800	lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA	820
Db	1336	TGATCGGGGAGCAGCGGTACGATTCCCTGTCCAATGTAGCACCTTGGCAAGCTTCTCTG	1395	2416	AGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTTCCAGCCCTCTTCG	2475
QY	460	luProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaA	480	820	laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT	840
Db	1396	AGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTTGGTGTACATCTCTCCGAAAGCAG	1455	2476	CCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTGGCTACATTAAGAAATCCCT	2535
QY	480	laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP	500	840	yzAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnGlnG	860
Db	1456	CCCGAAGGCTGGCCAGGCTCTCTAGGGCTATAGGCGTTCAGGCTGGGCTGGCTCAGCAGCC	1515	2536	ACAACATCTTTGATGGTGTCTATTGTGGTCTCAGTGTGTGGGAGATTGTGGGCCAGCAGG	2595
				860	lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetMetArgValLeuLysLeuValArgP	880

Db	2596		GAGGTGGCCTGTTCGGTGTCTGGGACCTTCCGCCTGATGCGGTGCTGAAGCTGGTGGCT	2655
QY	880		heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT	900
Db	2656		TCCTGCCGGCCCTGCAGGCCAGCTCGTGGTGTCTTCATCTTCAGCATCTCTGGCATCATCTCT	2715
QY	900		hrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuP	920
Db	2716		CCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTCAGCATCTCTGGCATCATCTCT	2775
QY	920		heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA	940
Db	2776		TTGGTTGCAAGTTTCGATCTGAACGGGATGGGGACACGTTGCCAGACCCGGAAGATTTCG	2835
QY	940		spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL	960
Db	2836		ACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGATTCTGACTCAGGAAGACTGGAATA	2895
QY	960		ysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaL	980
Db	2896		AAGTCCTCTACAACGGCATGGCCTCCACATCGTCTGGCTGTCTTTTACTTTCATCGCC	2955
QY	980		euMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyP	1000
Db	2956		TCATGACTTTTGGCAACTATGTGCTCTTTAACCTGTGTGGTGGCCATTCTTTGTGGAAGGAT	3015
QY	1000		heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV	1020
Db	3016		TCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTTCGCCCAGTG	3075
QY	1020		alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG	1040
Db	3076		TGGATGGTGTATGGGGACAGAAAGACGCTTGGCCCTGGTGGCTTTGGGAGAACACGCGG	3135
QY	1040		luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH	1060
Db	3136		AACACGAAAGAGCCTTTTGGCACCCCTCATCATCATACGGCTGCGACACCAATGTAC	3195
QY	1060		isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrS	1080
Db	3196		ACCCCAAGAGCTCCAGCACAGGTGTGGGGAGCACTGGGCTCTGGCTCTCGACGTACCA	3255
QY	1080		erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerA	1100
Db	3256		GTAGCAGTGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAAATGTCCGCCAAGTG	3315
QY	1100		laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerS	1120
Db	3316		CCCGCAGCTCCCCGCAAGTCCCTGGAGTCCGGCAAGCAGCTGGACACGAGCGCTCCA	3375
QY	1120		erArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgA	1140
Db	3376		GCAGGAACAGCCTGGGCCGGGGCCCCCAGCCCTAAAGCGGAGGAGCCCGAGCGGGAGCGGA	3435
QY	1140		rgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerGluGluA	1160
Db	3436		GGTCCCTGCTGCTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAAGTTTCAGAAAGAGG	3495
QY	1160		spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL	1180
Db	3496		ACCGGGCCAGCCAGCAGCAGTGACCATCGCCACAGGGGTTCCTTGGAACGTGAGGCCA	3555
QY	1180		ysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG	1200
Db	3556		AGAGTTCTTTGACCTGCCTGACACTCTGCAGGTGCCGGGGCTGCACCGCACAGCCAGCG	3615
QY	1200		lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA	1220
Db	3616		GCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAAATGGCAAGTCCGCTTCAGGGCGTTTG	3675
QY	1220		laArgThrLeuArgThrAspProGlnLeuAspGlyAspAspAsnAspGluGlyA	1240

3676	CCC	GAC	CCCTGAGGAC	TGATGAC	CCCCCAACTGGATGGGATGATGAC	ATGATGAGGGAA	3735														
1240	snLeuSer	Lys	Gly	Glu	Arg	Ile	Gln	Ala	Trp	Val	Arg	Ser	Arg	Leu	Pro	Ala	Cys	Cys	A	1260	
3736	ATCT	GAG	CAAA	GGG	GAACG	CATACA	AGCCTGGG	TCAGATCCG	GCCTCC	TGCTGCT	GTGCT	GTGCT	GTGCT	GTGCT	GTGCT	GTGCT	GTGCT	GTGCT	GTGCT	3795	
1260	rgGlu	Arg	Asp	Ser	Trp	Ser	Ala	Tyr	Ile	Phe	Pro	Gln	Ser	Arg	Phe	Arg	Leu	Leu	C	1280	
3796	GAG	AGC	GAG	ATT	TCCT	GGT	CGCCTAT	ATCTTT	CTCTCT	CAGTCA	AGGTTTC	GTCT	CTCT	GT	3855						
1280	ysHis	Arg	Ile	Ile	Thr	His	Lys	Met	Phe	Asp	His	Val	Val	Leu	Val	Ile	Ile	Phe	Leu	A	1300
3856	GTC	ACCG	GATCAT	CACCC	ACA	AGATGTTT	GACCAT	GTGT	GGTCT	CTCGT	CAATCAT	CTT	CTCT	CA	3915						
1300	snCys	Ile	Thr	Ile	Ala	Met	Glu	Arg	Pro	Lys	Ile	Asp	Pro	His	Ser	Ala	Glu	Arg	Ile	P	1320
3916	ACT	GTAT	CACCAT	CGCT	ATGAG	GCGCC	CAAAATTG	ACCC	CCACAG	CGCTGAG	CGCATCT	3975									
1320	heLeu	Thr	Leu	Ser	Asn	Tyr	Ile	Phe	Thr	Ala	Val	Phe	Leu	Ala	Glu	Met	Thr	Val	Lys	V	1340
3976	TCCT	GAC	CTCT	CCAACT	ATACAT	CTTCA	CGCAG	CTTTT	CTAGCT	GAAATG	ACAGTGA	AGG	4035								
1340	alVal	Ala	Leu	Gly	Trp	Cys	Phe	Gly	Glu	Gln	Ala	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	Val	L	1360
4036	TGGT	GGCACT	GGGCTGGT	GTGCTTT	GGGAG	CAGG	CCCTAC	CTGCG	CAGCAG	CTGGA	ATGTGC	4095									
1360	euAsp	Gly	Leu	Leu	Val	Leu	Ile	Ser	Val	Ile	Asp	Ile	Leu	Val	Ser	Met	Val	Ser	Asp	S	1380
4096	TGG	ACG	CTT	GTGT	GTCTCAT	CTCGT	CATCG	ACATCCT	GGTCT	CCATGGT	CTCCG	GACA	4155								
1380	erGly	Thr	Lys	Ile	Leu	Gly	Met	Leu	Arg	Val	Leu	Arg	Leu	Leu	Arg	Thr	Leu	Arg	Pro	L	1400
4156	GCGG	CAACA	GATCCT	TGG	CATGCT	GAGGT	GTCTG	CGGCT	GTCTG	CGGAC	CTGCGT	CCAC	4215								
1400	euArg	Val	Ile	Ser	Arg	Ala	Gln	Gly	Leu	Lys	Leu	Val	Val	Glu	Thr	Leu	Met	Ser	Ser	L	1420
4216	TCAG	GTTCAT	CAGCC	GGGCC	CAGG	CACTGAA	AGCTGGT	GGTAG	AGACTCT	GTATGT	CATCCC	4275									
1420	euLys	Pro	Ile	Gly	Asn	Ile	Val	Val	Ile	Cys	Cys	Ala	Phe	Phe	Ile	Ile	Phe	Gly	Ile	L	1440
4276	TCAA	ACCCAT	TGGCA	ACATT	GTGGT	CAATT	TGCTGT	GCCTTCTT	TCATCA	ATTTT	TGGAATTC	4335									
1440	euGly	Val	Gln	Leu	Phe	Lys	Gly	Lys	Phe	Val	Cys	Gln	Gly	Glu	Asp	Thr	Arg	Asn	I	1460	
4336	TCG	GGGTGC	AGCTCTT	CAA	GGGAAGT	TTCTT	CGTGT	TCAGG	GTGAGG	ACAC	CACAGGA	ACA	4395								
1460	leThr	Asn	Lys	Ser	Asp	Cys	Ala	Glu	Ala	Ser	Tyr	Arg	Trp	Val	Arg	His	Lys	Tyr	Asn	P	1480
4396	TCAC	TAA	CAAAAT	CCGACT	GCGCT	GAGCC	CAGCTAC	CGATGGG	TCCGG	CTCC	CAAGTACA	CAACT	4455								
1480	heAsp	Asn	Leu	Gly	Gln	Ala	Leu	Met	Ser	Leu	Phe	Val	Leu	Ala	Ser	Lys	Asp	Gly	Trp	V	1500
4456	TTG	ACAACT	TGGCC	AGGCTCT	GATGT	CCCTG	TTTGT	GTCTGG	CCCTCC	CAAGAT	TGTTGGG	4515									
1500	alAsp	Ile	Met	Tyr	Asp	Gly	Leu	Asp	Ala	Val	Gly	Val	Asp	Gln	Gln	Pro	Ile	Met	Asn	H	1520
4516	TTG	ACATCAT	GTATGAT	GGGTGG	ATGCTGT	GGGTGG	ATGATCAG	CAGC	AGCCCAT	CATGA	ACC	4575									
1520	isAsn	Pro	Trp	Met	Leu	Leu	Tyr	Phe	Ile	Ser	Phe	Leu	Leu	Ile	Val	Ala	Phe	Phe	Val	L	1540
4576	ACA	ACCCCT	GGATGCT	GTATAC	TTTCA	TCTCCT	CTCAT	CGTGG	CCCTTCT	TTGTCC	4635										
1540																					

QY 1600 heArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyV 1620
Db 4816 TCCGGCTCCTTGTCACACACCTGTGTACAGCCACTACCTGGACCTCTTCATCACTGGTG 4875
QY 1620 alileGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA 1640
Db 4876 TCATCGGGCTGAACGTGGTCACTATGGCCATGGAAACATTACAGAGCCCCAGATCCTGG 4935
QY 1640 spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP 1660
Db 4936 ACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTCTTGTCTTTGAGTCAGTT 4995
QY 1660 heLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAspL 1680
Db 4996 TCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTCCAGGACACAGGTGGAACCCAGCTGGACC 5055
QY 1680 euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS 1700
Db 5056 TGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGT 5115
QY 1700 erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL 1720
Db 5116 CGCTGCCCATCAACCCCAACCATCATCCGTATCATGAGGTGCTCCGATTTGCTCGAGTTC 5175
QY 1720 euLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL 1740
Db 5176 TGAAGCTGTTGAAGATGGCTGTGGCATGCGGGCACTGCTGCACACGGTGATGCAGGCC 5235
QY 1740 euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL 1760
Db 5236 TGCCCCAGGTGGGAACCTGGCACTTCTCTTCAATGTTATTGTTTTTCACTTTGTCAGCTC 5295
QY 1760 euGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG 1780
Db 5296 TGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGG 5355
QY 1780 lyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT 1800
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QY 1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT 1820
Db 5416 CTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCCGGGACTGTGACAGGAGTCCA 5475
QY 1820 hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP 1840
Db 5476 CCTGTACAAACACTGTCACTCCCTATCTACTTTGTGTCCTTCGTGCTGACGGCCAGT 5535
QY 1840 heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysG 1860
Db 5536 TTGTGCTGGTCAACGTGGTCACTAGCTGTGCTGATGAACACCTGGAAGAAAGCAACAAG 5595
QY 1860 luAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerP 1880
Db 5596 AGGCCAAGGAGGAGGCGGAGCTCGAGGCGGAGCTGGAGCTGGAGATGAAGACGCTCAGCC 5655
QY 1880 roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS 1900
Db 5656 CGCAGCCCCACTCCCGCTGGGCGAGCCCTTCTCTGGCCGGGGTGGAGGGTGTCAACA 5715
QY 1900 erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG 1920
Db 5716 GTACTGACAGCCCTAAGCCTGGGCTCCACACACCACTGCCACATTGGAGCAGCTCGG 5775
QY 1920 lyPheSerLeuGluHisProThrMetValProHisProGluValProValProLeuG 1940
Db 5776 GCTTCTCCCTTGAGCACCCCAACGATGTTACCCACCCCGAGGAGGTGCCAGTCCCCCTAG 5835
QY 1940 lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA 1960
Db 5836 GACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCCCCAATG 5895

QY 1960 spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG 1980
Db 5896 ACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGTGG 5955
QY 1980 lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS 2000
Db 5956 GGCTCCCCAAAGCCAGTCAAGCTCCATCTTGTCCGTTCACTCCCAACCCAGACACCA 6015
QY 2000 erCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProT 2020
Db 6016 GCTGCATCTACAGCTTCCCAAGATGTGCACATATCTCTCCAGCTCATGGGCTCCCA 6075
QY 2020 hrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProL 2040
Db 6076 CCTGGGCGGCATCCCTAAACTACCCCCACCTGGCGCTCCCTCTGGCTCAGAGGCCTC 6135
QY 2040 euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG 2060
Db 6136 TCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGCCGG 6195
QY 2060 luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT 2080
Db 6196 AAGACCTGTTGTACAGGTGAGTGGGCCCTCTCTGCCCTCTGACCCGGTCTCATCTTCT 6255
QY 2080 rpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysH 2100
Db 6256 GGGCGGGTCCAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAGC 6315
QY 2100 isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG 2120
Db 6316 ACATCCGCTGCCAGCCCCCTTGGCCAGGCCTGGAACCCAGCTGGGCCAAGGACCTCCAG 6375
QY 2120 luThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuP 2140
Db 6376 AGACCAGAGCAGCTTAGAGCTGGACAGGAGCTGAGCTGGATTTTCAGGAGACCTCCTTC 6435
QY 2140 roSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluT 2160
Db 6436 CCAGCAGCCAGGAAGAACCCCTGTTCCACGGGACCTGAAGAAGTGCTACAGTGTAGAGA 6495
QY 2160 hrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleA 2180
Db 6496 CCAGAGCTGCAGGCGCAGGCCTGGGTCTTGGCTAGATGAACAGCGGAGACACTCCATTG 6555
QY 2180 laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG 2200
Db 6556 CTGTCACTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCAAGCCCCCTCAAGCCTCG 6615
QY 2200 lyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerI 2220
Db 6616 GGGGCCAACCTCTTGGGGTCTTGGGAGCGGCGCTTAAGAAAAAACTCAGCCCCACCCAGTA 6675
QY 2220 leSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysL 2240
Db 6676 TCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCACTCCTGGTGTCTGCC 6735
QY 2240 euArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAsps 2260
Db 6736 TCAGGAGGAGGGCGCGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACA 6795
QY 2260 erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSera 2280
Db 6796 GCAGGCTGCCTCACCTCCCCAAAGAAAGACACGCTGAGTCTCTGGTTTGTCTTCTG 6855
QY 2280 spProThrAspMetAspPro 2286
Db 6856 ACCCAACAGACATGGACCCC 6875

RESULT 3
AAZ52309
ID AAZ52309 standard; cDNA; 7286 BP.
XX XX
AC AAZ52309;

XX 18-JUL-2000 (first entry)
XX Rat pancreatic T-type calcium channel cDNA.
XX
KW Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
KW pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; L type calcium channel; NIDDM;
KW type II diabetes; non-insulin dependent diabetes mellitus; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .157
FT /*tag= b
FT /note= "Region upstream to the coding region of
FT pancreatic T-type calcium channel protein"
FT 2. .7285
FT /*tag= a
FT /product= "Pancreatic T-type calcium channel alpha1
FT subunit"
FT /transl_except= (pos:11. .13, aa:Xaa)
FT /transl_except= (pos:7022. .7024, aa:Xaa)
FT /transl_except= (pos:7112. .7114, aa:Xaa)
FT /note= "Xaa corresponds to in-frame stop codon. This
FT region includes sequence upstream to the coding region of
FT pancreatic T-type calcium channel protein. Does not
FT include stop codon"
FT /partial
FT 158. .7285
FT /*tag= c
FT /product= "Pancreatic T-type calcium channel alpha1
FT subunit"
FT /note= "This region is claimed as SEQ ID NO: 1"
XX
PN WO200015845-A1.
XX
PD 23-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019675.
XX
PR 26-AUG-1998; 98US-0098004P.
PR 27-JAN-1999; 99US-0117399P.
XX
PA (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
PI Li M;
XX
DR WPI; 2000-271475/23.
DR P-PSDB; AAY70720.
XX
PT Novel nucleic acids encoding pancreatic T-type calcium channels used for
PT regulation of T-type calcium channels and treatment of type II diabetes.
XX
PS Example 1; Page 114-119; 124pp; English.
XX
CC The present cDNA encodes a protein that includes pancreatic T-type
CC calcium channel alpha1 subunit derived from rat insulin secreting beta
CC cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-
CC type calcium channel alpha1 subunit (alpha1G). The T-type Ca2+ channel
CC from INS-1 (alpha1G-INS) and neuronal alpha1G are alternative splice
CC isoforms of the same gene. The INS-1 isoform is also expressed in brain,
CC neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+
CC channel belongs to the family of low voltage activated Ca2+ channels. The
CC present sequence is used for treating diseases associated with abnormal
CC expression or function of T-type calcium channels. They are especially
CC used for treating type II diabetes. Modulators of pancreatic T-type Ca2+
CC channel e.g. antisense oligonucleotides, ribozymes and inhibitors are
CC used in methods for modifying insulin secretion by pancreatic beta cells,
CC basal calcium levels, potential L type calcium channel activity,
CC pancreatic cell death, pancreatic beta cell proliferation and calcium
CC influx through L type calcium channels in cells
XX

SQ Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 7286
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 3 Gaps: 2
US-09-611-257A-24 (1-2287) x AA252309 (1-7286)
QY 1 MetLeuProHisArg-ValProArg-CysValArgThrProProLeuArgGlySerAlaA 20
DB 58 ATGCTCCCCACCGGGGTCCCCGGTTGCGTGAGGACACCTCCTCTGAGGGCTCCGCTC 117
QY 20 rgProSerSerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
DB 118 GCCCTCTTCGGACCCCGGGGCCCGGCTGGCCAGAGGATGGACGAGGAGGATGG 177
QY 40 luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProG 60
DB 178 AGCGGGCGCCGAGAGTCGGGACAGCCCCGTAGCTTCACGCAGCTCAACGACCTGTCCGG 237
QY 60 lyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGl 79
DB 238 GGCGGGGGCCGCGAGGGGGCGGGTGCACGGGAAAGGACCCCGGCGAGCGGACTCCGA 297
QY 79 uAlaGluGlyLeuProTyProAlaLeuAlaProValValPhePheTyLeuSerGlnAs 99
DB 298 GCGGAGGGGTGCCGTACCCGGCGGTAGCCCCGGTGGTTTTCTTCTACTTGAGCCAGGA 357
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119
DB 358 CAGCGCCCGCGAGGTGGTGTCTCCGACGGTCTGTAAACCCGTGGTTCGAGCGAGTCAG 417
QY 119 rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIl 139
DB 418 TATGCTGGTCAATCTTCTCAACTGTGTGACTCTGGGTATGTTTTCAGGCCGTGTGAGGACAT 477
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPh 159
DB 478 TGCCGTGTGACTCCCGAGCGTCCGGATCCTGCAGCCCTTCGATGACTTCATCTTTGCCTT 537
QY 159 ePheAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179
DB 538 CTTTGTGTGGAAATGGTGGTGAAGATGGTGGCTTGGGCATCTTTGGGAAGAAATGTTA 597
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTy 199
DB 598 CTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTTGATTCAGGAGATGCTGGAGTA 657
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219
DB 658 TTCGCTGGACCTGCAGAACGTGAGCTTCTCCGAGTCAGGACAGTCCGCTGTGCTGGACC 717
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh 239
DB 718 GCTCAGGGCCATTAAACCGGTGCCAGCATCGCATTCGTCACATTTACTGTGGACAC 777
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 259
DB 778 CTTGCCTATGCTGGGCAACGTCTGCTGCTCTGTTCTTCTGCTTTTTCATCTTTTGGCAT 837
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279
DB 838 CGTGGCGTCCAGCTGTGGGCGAGGACTGTCTTCGCAACCGATGCTTCTCCCGAGAACTT 897
QY 279 eSerLeuProLeuSerValAspLeuGluProTyTrpGlnThrGluAsnGluAspGluse 299
DB 898 CAGCCTCCCCCTGAGCGTGGACCTGGAGCCCTATTACAGACAGAGATGAGGACGAGAG 957
QY 299 rPropheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh 319

Db	958	CCCCCTTCATCTGCTCTCAGCCCTCGGGAGAAATGGCATGAGATCCTGCAGGAGTGTGCCAC	1017	Db	2038	GGCCTTCAGCTCCATGCACAAGCTCCTCGGAGACACAGAGTACGGAGCCTGCCATAGCTC	2097
QY	319	rLeuArgGlyGluGlyGlyGlyGlyProCysSerLeuAspTyrGluThrTyrAsnSe	339	QY	679	rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy	699
Db	1018	ACTGCGTGGGAAGCGGTGGTGGCCACCCTGCAGTCTGGACTATGAGACCTATAACAG	1077	Db	2098	CTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCCTGCGGGCCGGACAGTTG	2157
QY	339	rSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyG1	359	QY	699	sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs	719
Db	1078	TTCCAGCAACACCACCTGTGTCAACTGGAACAGTACTATACAACTGCTCTCGGGCGGA	1137	Db	2158	TCCTACTGTGCCCGACAGGAGCAGGAGAGCCAGAGTCCGCTGACCATGTTCATGCCTGA	2217
QY	359	uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaI1	379	QY	719	pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs	739
Db	1138	GCACAACCCCTTCAAGGCGCCATCAACTTGACAACATTGGCTATGGCTGGATCGCCAT	1197	Db	2218	CTCAGACAGCGAGGCTGTGTATGAGTTTCACACGAGCGCTCAGCACAGTGACCTCCGGGA	2277
QY	379	ePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHi	399	QY	739	pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle	759
Db	1198	CTTCCAGGTCAACACTGGAGGGCTGGGTGCACATCATGTACTTCGTAATGGACGCTCA	1257	Db	2278	TCCCCACAGCCGGCGGCAGACGCGGAGCCCTGGGCCCAGATGCAGAGCCTAGTTCTGTGCT	2337
QY	399	sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetI1	419	QY	759	uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG1	779
Db	1258	CTCCTTCTACAACTTCATCTACTTCATTCCTTCATCATCTCGTGGCTCCTTCTTCATGAT	1317	Db	2338	GGCTTCTGGAGGCTGATCTGTGACACATTCGCGAAGATCGTAGATAGCAAAATACTTTGG	2397
QY	419	eAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG1	439	QY	779	yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisG1	799
Db	1318	CAACCTGTGCCTGGTGGTGAATGCCACGCAGTTCTCCGAGACCAACAGCGGGAGAGTCA	1377	Db	2398	CCGGGGATCATGATCGCCATCCTGGTCAATACACTCAGCATGGCATGGCATACCACGA	2457
QY	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459	QY	799	uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh	819
Db	1378	GCTGATGGGGAGCAGCGTGTACGATTCTGTCCAATGCTAGCACCCCTGGCAAGCTTCTC	1437	Db	2458	GCAGCCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTTCCAGACCTCTT	2517
QY	459	rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl	479	QY	819	eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPropheGlyTyrIleLysAsnPr	839
Db	1438	TGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCCTCCGAAAAGC	1497	Db	2518	CGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTTGGCTACATTAAGAATCC	2577
QY	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499	QY	839	oTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnG1	859
Db	1498	AGCCCGAAGCTGGCCAGGTCTCTAGGGCTATAGGGGTGCGGGCTGGCTGCACGAC	1557	Db	2578	CTACAACATCTTGTGATGGTGTCTATGGTTCATCAGTGTGGGAGATTGTGGGCCAGCA	2637
QY	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519	QY	859	nGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr	879
Db	1558	CCCAGTGGCCGCTAGTGGGCAGGAGCCGCCAGCCAGTGGCAGCTGCACCTCACACCG	1617	Db	2638	GGGAGGTGGCCTGTCGGTGTGCGGACCTTCCGCCCTGATCGGGTGTGAAGCTGGTGCG	2697
QY	519	gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrHisLe	539	QY	879	gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl	899
Db	1618	TCGTCTGTCTCCACCCTGGTCCACCACCATCACACCACCATCACCACTACCACT	1677	Db	2698	CTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTATGAAGACCATGGACACCTGGC	2757
QY	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559	QY	899	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	1678	GGGTAATGGGACGCTCAGAGTTCCCGGGCCAGCCCGAGATCCAGGACAGGATGCCAA	1737	Db	2817	CACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTCAGCATCCTGGGCATGCATCT	2877
QY	559	nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr	579	QY	919	aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMethIse	919
Db	1738	TGGGTCTCGCCGGCTCATGCTACCAACCCCTCTACACCCACTCCCTCTGGGGGCCCTCC	1797	Db	2758	CACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTCAGCATCCTGGGCATGCATCT	2817
QY	579	oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr	599	QY	919	pPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	1798	GAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGCTGCCACTTGGAGCCAGTCCG	1857	Db	2818	CTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGACACGTTGCCAGACCGGAAGATTT	2877
QY	599	gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerG1	619	QY	939	eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs	959
Db	1858	TTGCCAGGCACCCCTCCAGATGCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGG	1917	Db	2878	CGACTCCCTGCTCTGGCCCATCGTCACTGCTTTTCAGATTCTGACTCAGGAAGACTGGAA	2937
QY	619	yLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639	QY	959	nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl	979
Db	1918	GAAGGTGTACCCCTGTGCATACCAGCCCTCCACCAGAGATACTGAAGGATAAAGCACT	1977	Db	2938	TAAAGTCTCTACACGGCATGGCCTCCACATCGTCTTTGGGCTGCTTTACTTTCATCGC	2997
QY	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG1	659	QY	979	aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG1	999
Db	1978	AGTGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCCTCACCACTTCAACATCCCACCTGG	2037	Db	2998	CCTCATGACTTTTGGCAACTATGTGCTCTTTAAACCTGCTGTGGTGGCCATCTTTGTGAAGG	3057
QY	659	yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe	679	QY	999	yPheGlnAlaGlu-----	1003
				Db	3058	ATTCAGGCAGAGGAAATCGGCAAAACGGGAAGATCGGAGTGGACAGTTAAGCTGTATTCA	3117
				QY	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePh	1016
				Db	3118	GCTGCCTGTCAACTCTCAGGGGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTT	3177

Qy 1016 eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuG1 1036
Db 3178 TTCGCCAGTGTGGATGGTATGGGACAGAAAGAGCGCTTGGCCCTGGTGGCTTTGGG 3237
Qy 1036 yGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaTh 1056
Db 3238 AGAACACGGGAACACTAGAAAGAGCCCTTTGGCCACCCCTCATCCATACGGCTGCGAC 3297
Qy 1056 rProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe 1076
Db 3298 ACCAATGTCACTACCCAGAGCTCCAGCACAGGTGTGGGGGAAGCACTGGGCTCTGGCTC 3357
Qy 1076 rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy 1096
Db 3358 TCGACGTACCAGTAGCAGTGGTCCGTGAGCCTGAGCCTGGAGCTGCCACCATGAGATGAAATC 3417
Qy 1096 sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1116
Db 3418 TCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGGCAAGCAGCTGGACCAG 3477
Qy 1116 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1136
Db 3478 CAGGCGCTCCAGCAGGAACAGCTGGCGCCGGCCCCCAGCCCTAAAGCGGAGAGCCCCGAG 3537
Qy 1136 rGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSe 1156
Db 3538 CGGGAGCGGAGGTCCCTGTCTGTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAG 3597
Qy 1156 rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuG1 1176
Db 3598 TTCAGAAAGAGGACCGGGCCAGCCAGCAGGAGTACCATCGCCACAGGGTTCTTTGGA 3657
Qy 1176 uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr 1196
Db 3658 ACGTGAGGCCAAGAGTTCTTTGACCTGCCTGACACTTGCAGGTGCCGGGGCTGCACCG 3717
Qy 1196 gThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSe 1216
Db 3718 CACAGCCAGCGCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTC 3777
Qy 1216 rGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAs 1236
Db 3778 AGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCAACTGGATGGGGATGATGACAA 3837
Qy 1236 nAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPr 1256
Db 3838 TGATAGGGAAATCTGAGCAAAAGGGAACGCATACAAGCCTGGGTGAGATCCCGGCTTCC 3897
Qy 1256 oAlaCysCysArgGluArgAspSerTrpSerAlaTyrllePheProProGlnSerArgPh 1276
Db 3898 TGCCTGTTCGCGAGAGCGAGATTCTGGTTCGGCCTATATCTTCTCCTCAGTCAAGGTT 3957
Qy 1276 eArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValI1 1296
Db 3958 TCGTCTCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTGTGCTCTCGTCAT 4017
Qy 1296 eIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAl 1316
Db 4018 CATCTTCCTCAACTGTATCACCATCGCTATGGAGCGGCCCAAAATTGACCCCCACAGCGC 4077
Qy 1316 aGluArgIlePheLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMe 1336
Db 4078 TGAGCGCATCTTCTGACCCCTCTCCAACCTACATCTTCACGGCAGTCTTTCTAGCTGAAAT 4137
Qy 1336 tThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlleuArgSerSe 1356
Db 4138 GACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTTGGGAGCAGGCCCTACCTGCGCAGCAG 4197
Qy 1356 rTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMe 1376
Db 4198 CTGGAATGTGTGGACGGCTTGTGTGTCTCATCTCCGTATCGACATCTCTGGTCTCCAT 4257

Qy 1376 tValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgTh 1396
Db 4258 GGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGGGTGTCTGGGCTGCTGCGGAC 4317
Qy 1396 rLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLe 1416
Db 4318 CCTGGTCCACTCAGGGTCATCAGCCGGGCCAGGACTGAAGCTGGTGGTAGAGACTCT 4377
Qy 1416 uMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleI1 1436
Db 4378 GATGTCATCCCTCAAAACCCATTGGCAACATTGTGTCATTGTCTGTGCTTCTTCATCAT 4437
Qy 1436 ePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAs 1456
Db 4438 TTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGTAGGGTGAGGA 4497
Qy 1456 pThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHi 1476
Db 4498 CACCAGGAACATCACTAAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGGCA 4557
Qy 1476 sLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLy 1496
Db 4558 CAAGTACAACCTTTGACAACTGGGCCAGGCTCTGATGTCCCTGTTGTGTGGCTTCCAA 4617
Qy 1496 sAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPr 1516
Db 4618 GGATGGTTGGTTGACATCATGTATGATGGGCTGGATGCTGTGGTGTGGATCAGCAGCC 4677
Qy 1516 oIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAl 1536
Db 4678 CATCATGAACCAACACCCCTGGATGCTGTATACTTCACTCTCTTCTCTCATCTGTTGGC 4737
Qy 1536 aPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgG1 1556
Db 4738 CTTCCTTTGTCTGAACATGTTTGTGGCGTGGTGGAGAACTTCCATAAGTCAGACA 4797
Qy 1556 nHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLy 1576
Db 4798 GCACCAGGAGGAGGAGGAGGCGAGGCGGCGGTGAGGAGAAGCGACTACGGAGGCTGGAGAA 4857
Qy 1576 sLysArgArg-----SerLysGluLysGlnMe 1585
Db 4858 AAAGAGAAGGAATCTAATGTGTGGACGATGTAATGTCTCCGGCAGCTCAGCCAGCGCTGC 4917
Qy 1585 tAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHi 1605
Db 4918 GTCAGAAGCCCAGTGCAGGCCCTACTACTCTGACTACTCGAGATTCCGGGCTCTTGTCCA 4977
Qy 1605 sHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVa 1625
Db 4978 CCACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGTTGTCTATCGGGCTGAACGT 5037
Qy 1625 lValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysI1 1645
Db 5038 GGTCACTATGGCCATGGAAACATTACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGAT 5097
Qy 1645 eCysAsnTyrllePheThrValIlePheValPheGluSerValPheLysLeuValAlaPh 1665
Db 5098 CTGCAATTACATCTTTACCGTCATCTTTGTCTTTGAGTCAGTTTTCAAACCTTGTGGCCTT 5157
Qy 1665 eAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLe 1685
Db 5158 TGGCTTCCGCCGTTTCTTCCAGGACAGGTGGAAACCAGCTGGACCTGGCTATTGTGCTTCT 5217
Qy 1685 uSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnPr 1705
Db 5218 GTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATGCTTCGCTGCCCATCAACCC 5277
Qy 1705 oThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMe 1725
Db 5278 CACCATCATCCGTATCATGAGGGTGTCTCCGCATTTGCTCGAGTTCTGAAGCTGTTGAAGAT 5337
Qy 1725 tAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAs 1745

Db	6418	CCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGC	6477
Qy	2105	aProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLe	2125
Db	6478	CCCTTGCCAGGCGCTGGAACCCAGCTGGCCCAAGGACCCCTCCAGAGACCAGAACGAGCTT	6537
Qy	2125	uGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluG1	2145
Db	6538	AGAGCTGGACACGAGCTGAGCTGGATTTCAGGAGACCTCCTCCAGCAGCCAGGAAGA	6597
Qy	2145	uProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgAr	2165
Db	6598	ACCCCTGTCCCCACGGGACCTGAAGAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCG	6657
Qy	2165	gArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAs	2185
Db	6658	CAGGCTGGGTCCCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGCTCAGCTGTCTGA	6717
Qy	2185	pSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG1	2205
Db	6718	CAGGCTGCCAACCCCGCCTATGTCCAAGCCCTCAAGCCTCGGGGCCAACCTCTTGG	6777
Qy	2205	yGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProPr	2225
Db	6778	GGGTCTGGGAGCGCGCCTAAGAAAAAACTCAGCCCAACCCAGTATCTCTATAGACCCCCC	6837
Qy	2225	oGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaPr	2245
Db	6838	GGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCTGCTGCTGCTCAGGAGGGCGCC	6897
Qy	2245	oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerPr	2265
Db	6898	GGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCTTGACAGCACGGCTGCCTCACC	6957
Qy	2265	oSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAs	2285
Db	6958	CTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCCAACAGACATGGA	7017
Qy	2285	pPro 2286	
Db	7018	CCCC 7021	
RESULT 4			
AXX83485			
ID	AXX83485	standard; cDNA; 6762 BP.	
XX	XX		
AC	AXX83485;		
XX	07-DEC-1999	(first entry)	
DT			
XX			
DE		Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a) cDNA.	
XX			
KW		Human; T-type voltage-gated calcium channel; membrane; pore; ion;	
KW		activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.	
XX			
OS		Rattus sp.	
XX			
PN	WO9929847-A1.		
XX			
PD	17-JUN-1999.		
XX			
PF	30-OCT-1998;	98WO-US023161.	
XX			
PR	05-DEC-1997;	97US-00985809.	
XX			
PA	(LOYO) UNIV LOYOLA CHICAGO.		
XX			
PI	Perez-Reyes E, Cribbs LL;		
XX			
DR	WPI; 1999-394972/33.		
DR	P-PSDB; AAY14590.		
XX			
PT		New T-type voltage-gated calcium channels.	

XX Disclosure; Page 67-76; 138pp; English.

PS

XX

CC This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	6762
Score:	11798.00	Matches:	2250
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	3
Query Match:	98.09%	Indels:	2
DB:	2	Gaps:	0

US-09-611-257A-24 (1-2287) x AAX83485 (1-6762)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53

Db 2 TGGACGAGGAGGATGGAGCGGCGCCGAGGAGTGGGACAGCCCCGTAGCTTCACGC 61

QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73

Db 62 AGCTCAACGACCTGTCCGGGCGGGGGCCGGCAGGGCGGGGTGCGACGGAAGGACC 121

QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyPrProAlaLeuAlaProValValP 93

Db 122 CGGGCAGCGGGA CTCCGAGCGGAGGGGCTGCCGTACCCGGCGGTAGCCCCGGTGGTTT 181

QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCTTCTACTTGAGCCAGGACAGCCGCCCGGAGTGGTGTCTCCGCACGGTGTGAACC 241

QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CGTGGTTCGAGCGAGTCAGTATGCTGGTTCATCTCTCAACTGTGTGACTCTGGGTATGT 301

QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153

Db 302 TCAGGCGGTGTGAGGACATTGGCTGTGACTCCCGCGCTGCCGATCCTTGAGGCCTTCG 361

QY 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTGGCCTCTTTGGTGTGGAATGGTGGTGAAGATGGTGGCCTTGGGCA 421

QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193

Db 422 TCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTCA 481

QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213

Db 482 TTGCAGGGATGCTGGAGTATTTCGTGGACCTGCAGAACGTCAGCTTCTCCGCGAGTCAGGA 541

QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCCGTGTGCTGCGACCGGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATTTCTCG 601

QY 233 alThrLeuLeuAspThrLeuProMetLeuGlyAenValLeuLeuLeuLeuCysPhePheV 253

Db 602 TCACATTACTGTGGACACCTTGCCATATGCTGGGCAACGTCCTGCTGCTGTTCTTCG 661

QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273

Db 662 TCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGCAGGACTGCTTCGCAACCGGT 721

QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyTrTyrGlnT 293

Db 722 GCTTCTCCCGAGAACTTCAGCCTCCCCCTGAGCGTGAGACCTGGAGCCTTATTACCAGA 781

QY 293 hrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArgS 313

Db 782 CAGAGAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGAT 841

QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333

Db 842 CCTGCAGGAGTGTCCCACTGCGTGGGAAGCGGTGGTGGCCACCCCTGCAGTCTGG 901

QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353

Db 902 ACTATGAGACCTATAACAGTTCAGCAACACCACCTGTGTCAACTGGAACCACTACTATA 961

QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373

Db 962 CCAACTGCTCTCGGGCGGAGACAAACCCCTTCAAAGGCGCCATCAACTTTGACAACATTG 1021

QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393

Db 1022 GCTATGCTGGATCGCCATCTTCCAGGTCACTCACACTGGAGGGTGGGTGACATCATGT 1081

QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413

Db 1082 ACTTCGTAATGGACGCTCACTCCTTCTACAACCTCATCTACTTCTTCTCATCATCG 1141

QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433

Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCGAGTTCTCCGAGA 1201

QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453

Db 1202 CCAAAACAGCGGGAGAGTCACTGATGCGGAGCAGCGGTGTACGATTTCCTGTCCAATGCTA 1261

QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473

Db 1262 GCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGTATGAGGAGCTACTCAAGTACCTGG 1321

QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493

Db 1322 TGTACATCTCCGAAAAGCAGCCCGAAGGCTGGCCAGGCTCTTAGGGCTATAGCGGTGC 1381

QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513

Db 1382 GGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGCAGGAGCCCCAGCCAGTGGCA 1441

QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533

Db 1442 GCTGCACCTCGCTCACACCGCTGCTGTCTGTCCACACACCTGGTCCACCACCATCACACC 1501

QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553

Db 1502 ACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCTCCGGGCCAGCCAGAGA 1561

QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt 573

Db 1562 TCCAGGACAGGGATGCCAATGGGTCTGCCGGGCTCATGTACCAACCACCTCTACACCCA 1621

QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CTCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTTACCATGTGACT 1681

QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613

Db	1682	GCACCTTGGAGCAGTCCGTTGGCCAGGCACCCCTCCAGATGCCCATCGAGGCATCTG	1741	Db	2762	TGACTCAGGAAGACTGGAATAAAGTCCTCTACAAAGGCATGGCCTCCACATCGTCTTGGG	2821
QY	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI	633	QY	973	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuV	993
Db	1742	GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGTACATCAGCCCTCCACCAGAGA	1801	Db	2822	CTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTCTCTTTAACTGTCTGG	2881
QY	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs	653	QY	993	alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP	1013
Db	1802	TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACTCACCA	1861	Db	2882	TGGCCATTCCTTGTGGAAGGATTCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAGC	2941
QY	653	exPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673	QY	1013	roAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV	1033
Db	1862	GCTTCAACATCCACCTGGGCCCTTCAGTCCATGCACAAGCTCCTGGAGACACAGAGTA	1921	Db	2942	CTGATTTCTTTTCGCCCAGTGTGGATGGTGTATGGGACAGAAAGACGCTTGGCCCTGG	3001
QY	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693	QY	1033	alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisT	1053
Db	1922	CGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAG	1981	Db	3002	TGGCTTTGGGAGAACACGCGGAACCTACGAAAGAGCCCTTTTGGCACCCCTCATCATCATA	3061
QY	693	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera	713	QY	1053	hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG	1073
Db	1982	CCTGGGGCCGGACAGTTGTCTCCCTACTGTGCCGGACAGGACGAGAGCCAGAGTCCG	2041	Db	3062	CGGCTGCGACACCAATGTCCACCCCAAGAGCTCCAGCACAGGTGTGGGGAAGCACTGG	3121
QY	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733	QY	1073	lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisG	1093
Db	2042	CTGACCATGTATGCCTGACTCAGACAGCGAGGCTGTATGATGATTCACACAGGACGCTC	2101	Db	3122	GCTCTGGCTCTCGACGTACAGTAGCAGTGGTCCGCTGAGCCTGGAGCTGCCACCATG	3181
QY	733	lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753	QY	1093	luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSers	1113
Db	2102	AGCACAGTGACCTCCGGATCCCAACAGCCGGCGGACAGCGGAGCCTGGGCCAGATG	2161	Db	3182	AGATGAATGTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGTGGGCAAGCA	3241
QY	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773	QY	1113	erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA	1133
Db	2162	CAGAGCCTAGTCTGTGTGGCTTTCTGGAGGCTGATCTGTACACATTCGCGAAGATCG	2221	Db	3242	GCTGGACAGCAGCGCTCCAGCAGGAACAGCCTGGGCCCGGCCCTAAAGCGGA	3301
QY	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793	QY	1133	rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG	1153
Db	2222	TAGATAGCAATACTTTGGCCGGGAATCATGATCGCCATCCTGTGTCAATACACTCAGCA	2281	Db	3302	GGAGCCCGAGCGGGAGCGGAGTCCCTGCTGTCTGGAGAGGGCCAGGAGTCAAGATG	3361
QY	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813	QY	1153	luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
Db	2282	TGGGCATCGAGTACCAACAGCAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACA	2341	Db	3362	AGGAGGAAAGTTCAGAAAGAGGACCGGGCCAGCCCGCAGCAGGCAGTGACCATGCCACAGGG	3421
QY	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833	QY	1173	lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG	1193
Db	2342	TCGTCTTACCAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCT	2401	Db	3422	GTTCTTGGAACTGAGGCCAAGAGTTCCTTTGACCTGCTGACACTCTGACGTGCCGG	3481
QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT	853	QY	1193	lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL	1213
Db	2402	TTGGCTACATTAGAATCCCTACAACATCTTGTATGGTGTCTATGTGTCATCAGTGTGT	2461	Db	3482	GGCTGCACCCGCACAGCCAGCGCGCGGAGCTCTGCCCTCTGAGCACCAAGACTGTATGGCA	3541
QY	853	rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873	QY	1213	ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA	1233
Db	2462	GGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGGTGCTGCGACCTTCCGCCCTGATGC	2521	Db	3542	AGTCGGCTTCAGGGCCTTTGGCCCGCACCTGAGGACTGTATGACCCCACTGGATGGGG	3601
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893	QY	1233	spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS	1253
Db	2522	GGGTGCTGAAGCTGGTGCCTTCTCGCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATGA	2581	Db	3602	ATGATGACAAATGATGAGGAAATCTGAGCAAAAGGGAAACGCATACAAGCCTGGGTGAGAT	3661
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913	QY	1253	erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG	1273
Db	2582	AGACCATGGACAACGTGGCCACCTTCTGATGCTCCTCATGCTGTATCTTTCATCTTCA	2641	Db	3662	CCCCGCTTCTGCTGCTGTCGCCGAGAGCGAGATTCCTGGTGGCCCTATATCTTCTCCTC	3721
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933	QY	1273	lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV	1293
Db	2642	GCATCTCTGGCATGTCATCTCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACGT	2701	Db	3722	AGTCAAGGTTCGTCTCTCTGTGTACCCGGATCATCACCCACAAGATGTTTGACCATGTGG	3781
QY	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953	QY	1293	alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspp	1313
Db	2702	TGCCAGACCGGAAGAATTTCCAGTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT	2761	Db	3782	TCCTCGTTCATCATCTTCTCAACTGTATCACCATGCTATGGAGCGGCCCAAAATTGACC	3841
QY	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973	QY	1313	roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL	1333
				Db	3842	CCACAGCGCTGAGCGCATCTTCTCTGACCCCTCTCCAACTACATCTTCACGCGAGTCTTTC	3901

Qy 1333 euAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrL 1353
Db TAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTTGGGGAGCAGGCCTACC 3961
Qy 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
Db TGGCAGCAGCTGGAATGTGTGGACGGCTTGTGTGTCTCATCTCCGTATCGACATCC 4021
Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db TGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGTGCGGC 4081
Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db TGCTGCGGACCCCTGCGTCCACTCAGGGTCATCAGCGGGCCAGGGACTGAAGCTGGTGG 4141
Qy 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlap 1433
Db TAGAGACTCTGATGTATCCCTCAAACCCATTGGCAACATTGTGGTCAATTGTGTGCCT 4201
Qy 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db TCITTATCATTTTGGAAITCTCGGGGTGCAGCTCTTCAAAGGGAAGTCTTCGTGTGTC 4261
Qy 1453 lnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473
Db AGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCAGCTACCCGAT 4321
Qy 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db GGGTCGGGCACAAAGTACAACCTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTGTGC 4381
Qy 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db TGGCCTCCAAGGATGTTGGGTTGACATCATGTATGATGGGTGGATGCTGTGGGTGG 4441
Qy 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
Db ATCAGCAGCCCATCATGAACCAACAACCCCTGGATGCTGTATATCTTTCATCTCCTTCC 4501
Qy 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db TCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGCGTGGTGGTGGAGAACTTCCATA 4561
Qy 1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
Db AGTGACAGACAGACCAGGAGGAGGAGGCGGAGGCGCGTGGAGAGAGCGACTACGGA 4621
Qy 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProt 1593
Db GGCTGAGAAAAAGAGAGGAGTAAGGAGAGCAGATGGCCGGAAGCCAGCTGCAAGCCCT 4681
Qy 1593 yrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL 1613
Db ACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACC 4741
Qy 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633
Db TGGACCTCTTCATCACTGGTGTCTATCGGGCTGAACGTGGTCACTATGGCCATGGAAACATT 4801
Qy 1633 yrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1653
Db ACCAGCAGCCCCAGATCCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCA 4861
Qy 1653 lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673
Db TCCTTGTCTTTGAGTCAGTTTCAAACCTTGTGGCCTTGGCTTCCGCCGTTTCTTCCAGG 4921
Qy 1673 spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693
Db ACAGGTGGAACCAAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGG 4981

Qy 1693 luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713
Db AGGAGATTGAGGTCAATCTGTCTGCTGCCATCAACCCACCATCATCCGTATCATGAGG 5041
Qy 1713 alLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733
Db TGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGCATGCGGCACTGC 5101
Qy 1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
Db TGCACACGGTGTATGAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTTTCATGTTAT 5161
Qy 1753 euPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773
Db TGTITTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGA 5221
Qy 1773 hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
Db CACACCCCTTGTAGGGCTTGGGTGCGCATGCCACCTTTAGGAACCTTTGGTATGGCCTTTC 5281
Qy 1793 euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813
Db TGACCCCTCTTCCGAGTCTCCACTGGTGACAACCTGGAATGGTATTATGAAGGACACCCCTCC 5341
Qy 1813 rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS 1833
Db GGGACTGTGACCAGGACTCCACCTGCTACAACACTGTCTATCTCCCTATCTACTTTGTGT 5401
Qy 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853
Db CCTTCGTGCTGACGGCCAGTTTGTGTGGTCAACGTGGTTCATAGTGTGCTGATGAAGC 5461
Qy 1853 isLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuL 1873
Db ACCTGGAAGAAAGCAAAAGAGGCCAAGGAGGCGCGAGCTCGAGGCGGAGCTGGAGC 5521
Qy 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPropheLeuTrpP 1893
Db TGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGGCGAGCCCTTCTCTCTGGC 5581
Qy 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
Db CCGGGTGGAGGGTGTCAACAGTACTACAGCCCTAAGCCTGGGCTCCACACCACTG 5641
Qy 1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933
Db CCCACATTGGAGCAGCTCGGGCTTCTCCCTTGAGCACCCACCATGGTGTACCCACCCCG 5701
Qy 1933 luGluValProValProLeuGlyProAspLeuThrValArgLysSerGlyValSera 1953
Db AGGAGGTGCCAGTCCCCCTAGGACCAGACTGCTGACTGTGAGGAAGTCTGGTGTGAGCC 5761
Qy 1953 rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS 1973
Db GGACGCACCTCTTGCCCAATGACAGCTACATGTGCCCAATGGGAGCACTGCTGAGAGAT 5821
Qy 1973 erLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993
Db CCTTAGGACACAGGGCTGGGGCTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTTC 5881
Qy 1993 isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL 2013
Db ACTCCCAACCAGCAGACACAGCTGCATCTCTACAGCTTCCCAAAGATGTGCACATATCTGC 5941
Qy 2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgS 2033
Db TCCAGCCTCATGGGGCTCCACCTGGGGCGGCATCCCTAAACTACCCCCACCTGGCCGCT 6001
Qy 2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053
Db CCCCTCTGGCTCAGAGGCCTCTCAGGGCGCCAGGAGCAATAAGGACTGACTCCCTGGATG 6061
Qy 2053 alGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073

Db 6062 TGCAGGGCCTGGGTAGCCGGAGACCTGTTGTACAGGTGAGTGGCCCTCTGCCCTC 6121
QY 2073 euThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093
Db 6122 TGACCCGGTCTCATCTCTTGGGGCGGTTCAGCATTCAGGTGCAGCAGCGTTCCGGCA 6181
QY 2093 leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
Db 6182 TCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCTTGCCACAGGCTGGAACCCA 6241
QY 2113 erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
Db 6242 GCTGGGCCAAGGACCTCTCCAGAGACCAGAACGACGCTTAGAGCTGGACACGGAGTGAGCT 6301
QY 2133 rPileSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL 2153
Db 6302 GGATTTTCAGGAGACCTCTCTCCAGCAGCAGCAGGAAGAACCCCTGTTCACACGGGACCTGA 6361
QY 2153 ySLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspG 2173
Db 6362 AGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGGTTCTGGCTAGATG 6421
QY 2173 luGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuC 2193
Db 6422 AACAGCGGAGACACTCCATTGCTGTCTGCTGTGTGACAGCGGCTCCCAACCCCGCCTAT 6481
QY 2193 ysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysL 2213
Db 6482 GTCCAAGCCCTCAAGCCTCGGGGCCAACCTCTTGGGGTCTCTGGAGCCGGCCTAAGA 6541
QY 2213 ySLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProp 2233
Db 6542 AAAAACTCAGCCACCCAGTATCTATAGACCCCGGAGAGCCAGGCTCTCGGCCCC 6601
QY 2233 roCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProS 2253
Db 6602 CATGCAGTCTGGTGTCTGCCTCAGGAGGAGGGCGCGCCAGTACTAAGGATCCCT 6661
QY 2253 erValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeus 2273
Db 6662 CGGTCTCCAGCCCTTGACAGCAGGCTGCCTCACCTCCCCCAAGAAAGACACACGCTGA 6721
QY 2273 erLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6722 GTCTCTCTGGTTGTCTTCTGACCCCAACAGACATGGACCCC 6762

RESULT 5
AAX83487
ID AAX83487 standard; cDNA; 6816 BP.
AC AAX83487;
XX 07-DEC-1999 (first entry)
DT Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c) cDNA.
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
KW Rattus sp.
XX WO9929847-A1.
PN 17-JUN-1999.
PD 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
PR (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.
DR P-PSDB; AAY14592.
XX New T-type voltage-gated calcium channels.
PT Disclosure; Page 85-94; 138pp; English.
XX This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;
SQ

Alignment Scores: Length: 6816
Pred. No.: 0 Matches: 2248
Score: 11767.00 Conservative: 0
Percent Similarity: 98.90% Mismatches: 5
Best Local Similarity: 98.90% Indels: 20
Query Match: 97.83% Gaps: 1
DB: 2

US-09-611-257A-24 (1-2287) x AAX83487 (1-6816)
QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGGATGGAGCGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73
Db 62 AGCTCAACGACCTGTCCGGGGCCGGGGCCGGGCGGAGGTCGACGGAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCGGGCGTAGCCCCGGTGT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCCGCCGGAGCTGGTGTCTCCGCACGGTCTGTAACC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CGTGGTTCGAGCGAGTCAGTATGCTGGTCTTCTCACTGTGTGACTCTGGGTATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCAGGCGGTGTGAGGACATTCCTGTGACTCCAGCGCTCCCGATCCTGCAGGCTTCG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTTGCCCTTCTTTGCTGTGGAATAAGTGGTGAAGATGGTGGCTTGGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TTGCAGGGATGCTGGAGTATTCGCTGGACCTTGACACGTCAGCTTCTCCGAGTCAGGA 541

QY	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
Db	542	CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGATTCTCG	601
QY	233	alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuCysPhePheV	253
Db	602	TCACATTACTGCTGGACACCTTGCCATATGCTGGGCAACGTCTCTGCTGCTCTGTCTTCG	661
QY	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGCAGGACTGCTTCGCAACCGGT	721
QY	273	ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722	GCTTCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCCTATTACCAGA	781
QY	293	hrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGAGAT	841
QY	313	erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGCAGGAGTGTGCCACACTGCGTGGGAAAGCGGTGGTGGCCCAACCTTGAGTCTGG	901
QY	333	spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
Db	902	ACTATGAGACCTATAACAGTTCCAGCAACACCACTGTGTCAACTGGAACCACTACTATA	961
QY	353	hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG	373
Db	962	CCAACTGCTCTGCGGCGAGCACAAACCCCTTCAAAGGCGCCATCAACTTTGACAACATTG	1021
QY	373	lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT	393
Db	1022	GCTATGCTTGATCGCATCTTCCAGGTTCATCACACTGGAGGGCTGGTTCGACATCATGT	1081
QY	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV	413
Db	1082	ACTTCGTAATGGACGCTCACTCCTTCTACAACCTCATCTACTTCTTCTCTCATCATCG	1141
QY	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGAGTTCCTCGAGA	1201
QY	433	hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS	453
Db	1202	CAAAACAGCGGAGAGTCAGCTGATCGGGAGCAGCGTGATGCCACGAGTTCCTGTCCAATGCTA	1261
QY	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuV	473
Db	1262	GTACCTTGGCAAGCTTCTCTGAGCCAGGACGCTGCTATGAGGAGCTACTCAAGTACCTGG	1321
QY	473	alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTACATCCTCCGAAAAGCAGCCCCGAGGCTGGCCCCAGGTCTCTAGGGCTATAGCGGTGC	1381
QY	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGCTGCTCAGAGCCCCAGTGGCCCCGTAGTGGGCGAGGAGCCCCAGCCAGTGGCA	1441
QY	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
Db	1442	GCTGCACCTCGCTCACACCGTCGTCTGTCTGCCACCACTGGTCCACCACCATCACCCACC	1501
QY	533	isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCAGAGA	1561
QY	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT	573
Db	1562	TCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTCTACCACTCACCCCTACACCCA	1621

QY	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
DB	1622	CTCCCTCTGGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCTTACCATGCTGACT	1681
QY	593	ysHisLeuGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerG	613
DB	1682	GCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGAGGCATCTG	1741
QY	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI	633
DB	1742	GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAGA	1801
QY	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProThrLeuThrS	653
DB	1802	TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCGCAGCCCTGGGCCCCCACTCACCA	1861
QY	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
DB	1862	GCTTCAACATCCCACTGGGCCCTTCAGTCCATGCACAAGCTCCTGGAGACACAGAGTA	1921
QY	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
DB	1922	CGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAG	1981
QY	693	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyProGluSerA	713
DB	1982	CCTGGGGCCGGACAGTTGTCTCCTACTGTGTCCGGACAGGAGCAGGAGCCAGAGTCCG	2041
QY	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
DB	2042	CTGACCATGTCTATGCCTGACTCAGACAGCGAGGTGTGTATGATTTCACAGGACGCTC	2101
QY	733	lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA	753
DB	2102	AGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGACAGCGGAGCCTGGGCCCAGATG	2161
QY	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
DB	2162	CAGAGCCTAGTTCTGTGTGGCTTTCTGGAGGTGATCTGTGACACATTCGCGAAGATCG	2221
QY	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
DB	2222	TAGATAGCAAAATACTTTGGCCGGGGAATCATGATGCCCATCTCTGGTCAATACACTCAGCA	2281
QY	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
DB	2282	TGGGCATCGAGTACCACGACGAGCCCGAGGAGCTCACCAACGCCCTGGGAATCAGCAACA	2341
QY	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
DB	2342	TCGTCTTACCAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCT	2401
QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
DB	2402	TTGGTTCATTAAGAAATCCCTACAACATCTTTGATGGTGTCTATTGTGGTTCATCAGTGTGT	2461
QY	853	rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
DB	2462	GGGAGATTGTGGGCCAGCAGGGAGGTGGCCCTGTCTGGTGTCTGGGACCTTCGCCCTGATGC	2521
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
DB	2522	GGGTGTGAAGCTGGTGGCTTCTTCGCCGCCCTGCGAGCGCCAGCTCGTGTGCTCATGA	2581
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheS	913
DB	2582	AGACCATGGACAACGTGGCCACCTTCTGCATGTCTCCTCATGCTGTTTCATCTTCATCTTCA	2641
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
DB	2642	GCATCTCTGGGCATGCATCTCTTTGGTTGCAAGTTCCGATCTGAACCGGGATGGGACACGT	2701
QY	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953

Db 2702 TGCCAGACCGGAAGAAATTTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGATTCTC 2761
Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpA 973
Db 2762 TGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGGG 2821
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2822 CTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGTGG 2881
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
Db 2882 TGGCCATTCTTGTGGAGGATTCCAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGAGC 2941
Qy 1013 roAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV 1033
Db 2942 CTGATTTCTTTTCGCCCCAGTGTGGATGGTGATGGGACAGAAAGAGCGCTTGGCCCTGG 3001
Qy 1033 alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisT 1053
Db 3002 TGGCTTTGGGAGAACACCGCGAACTACGAAAGAGCCTTTTGGCCACCCCTCATCATCCATA 3061
Qy 1053 hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG 1073
Db 3062 CGGCTGGCACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGAGCACTGG 3121
Qy 1073 lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisG 1093
Db 3122 GCTCTGGCTCTCGACGTACCACTACCAAGAGCTCCAGCAGCTCGGCTGAGCCTGGAGCTGCCACCATG 3181
Qy 1093 luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
Db 3182 AGATGAATGTCCGCCAAGTGGCCGAGCTCCCGCACAGTCCCTGGAGTGGCGCAAGCA 3241
Qy 1113 erTirpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
Db 3242 GCTGGACCCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCGGGCCCCAGCCTAAAGCGGA 3301
Qy 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGlnAspG 1153
Db 3302 GGAGCCCGAGCGGGAGCGGAGGTCCCTGTCTGTGGAGAGGGCCAGGAGTCAAGATG 3361
Qy 1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
Db 3362 AGGAGGAAGTTCAGAGAGGACCGGGCCAGCCAGCCAGGAGTCAAGTCAAGTCAAGG 3421
Qy 1173 lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
Db 3422 GTTCCTTGGAACTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGACAGTCCGG 3481
Qy 1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
Db 3482 GGCTGCACCGCACAGCCAGCGCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGCA 3541
Qy 1213 ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3542 AGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCCACTGGATGGG 3601
Qy 1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTirpValArgS 1253
Db 3602 ATGATGACAATGATAGGGGAAATCTGAGCAAAGGGGAACGCACACAAGCCTGGGTCA 3661
Qy 1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
Db 3662 CCCGGCTCTCTGCCTGTGTCCGAGAGCGAGATTCTCTGGTGGCCCTATATCTTTCTCTC 3721
Qy 1273 lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
Db 3722 AGTCAAGGTTTCGTCTCTCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTGG 3781
Qy 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313

Db 3782 TCCTCGTCATCATCTTCTCAACTGTATCACCATCGTATGGAGCGCCCCAAATTGACC 3841
Qy 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
Db 3842 CCCACAGCGCTGAGGCGATCTTCTTGACCCCTCTCCAACCTACATCTTCACGGCAGTCTTC 3901
Qy 1333 euAlaGluMetThrValLysValValAlaLeuGlyTirpCysPheGlyGluGlnAlaTyrL 1353
Db 3902 TAGCTGAAATGACAGTGAAGTGTGGTGGCACTGGGCTGGTGTCTCATCTCCGTCAATCC 3961
Qy 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
Db 3962 TGGCAGCAGCTGGAAATGTGTGGACCGCTTGGTGTCTCATCTCCGTCAATCCGACATCC 4021
Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db 4022 TGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCTTGGCATGCTGAGGTGTCTCGGC 4081
Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db 4082 TGCTGGGACCCCTGCGTCCACTCAGGGTCAATCAGCCGGCCAGGACTGAAGTGTGG 4141
Qy 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaP 1433
Db 4142 TAGAGACTCTGATGTATCCCTCAAAACCCATTGGCAACATTTGTGGTCATTTGCTGTGCCT 4201
Qy 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db 4202 TCTTTCATCATTTTGGAAATTTCTCGGGGTGCAGCTCTTCAAAGGGAAGTCTTCTCGTGTGC 4261
Qy 1453 lnGlyGluAspThrArgAsnIleThrAsnLysSerSerAspCysAlaGluAlaSerTyrArgT 1473
Db 4262 AGGTGAGGACACAGGAACATCACTAACAAAATCCGACTGCGCTGAGGCCAGCTACCGAT 4321
Qy 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4322 GGGTCCGGCACAAGTACAACITTTGACAACTTGGCCAGGCTCTGTATGTGGTGTGGTGTGC 4381
Qy 1493 euAlaSerLysAspGlyTirpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db 4382 TGGCCTCCAAAGGATGGTGGGTGACATCATGTATGATGGCTGGATGTCTGGGTGTGG 4441
Qy 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
Db 4442 ATCAGCAGCCCATCATGAACCAACACCCCTGGATGTCTGTATATACTTTCATCTCTCTCC 4501
Qy 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4502 TCATCGTGGCCTTCTTTGTCTCTGAACATGTTTGTGGCGGTGGTGGAGAACTTCCATA 4561
Qy 1553 ysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
Db 4562 AGTCAGACAGCACAGGAGGAGGAGGAGGCGGCGGCGGCGGTGAGGAGAAAGCTACCGA 4621
Qy 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAla----- 1586
Db 4622 GGCTGGAGAAAAAGAGAAAGAGAGTAAGGAGAACAGATGGCCGATCTAATGTTGGACGATG 4681
Qy 1587 -----GluAlaGlnCysLysProTyrTyrS 1595
Db 4682 TAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAAGAGCCAGTCAAGCCCTACTACT 4741
Qy 1595 erAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspL 1615
Db 4742 CTGACTACTCGAGATTCCGGCTCCTTGTCCACCACTGTGTATCCAGCCACTACCTGGACC 4801
Qy 1615 euPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnG 1635
Db 4802 TCTTCATCACTGGTGTATCGGGCTGAACGTGTGCTATGGCCATGGAAACATTACCAGC 4861
Qy 1635 lnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheV 1655
Db 4862 AGCCCCAGATCTCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTTTTG 4921

Qy 1655 alPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgT 1675
Db TCTTTGAGTCAGTTTTCAAACTTGTGGCCTTGGCTTCCGCGTTTCTTCCAGGACAGGT 4981
Qy 1675 rpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluI 1695
Db GGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGA 5041
Qy 1695 leGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuA 1715
Db TTGAGGTCAATCTGTCTGCTGCCCATCAACCCACCATCATCCGTATCATGAGGTGCTCC 5101
Qy 1715 rgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisT 1735
Db GCATTGCTCGAGTCTGAAGCTGTGAAGATGGCTGTGGGCATCGGGCACTGCTGCACA 5161
Qy 1735 hrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
Db CGGTGATGCAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTCTCATGTTATTGTTT 5221
Qy 1755 heIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisP 1775
Db TCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACC 5281
Qy 1775 roCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
Db CTTGTGAGGCTTGGGTGGCATGCCACCTTTAGGAACCTTGGTATGGCCTTCTTGACCC 5341
Qy 1795 eupheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspC 1815
Db TCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCCGGGACT 5401
Qy 1815 ysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheV 1835
Db GTGACCAGGAGTCCACCTGTCTACACACTGTCTATCTCCCTATCTACTTTGTGTCCTCG 5461
Qy 1835 alLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuG 1855
Db TGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGTGATGAAGCACCTGG 5521
Qy 1855 luGluSerAsnLysGluAlaLysGluGluAlaGluLeuAlaGluLeuGluGluM 1875
Db AAGAAAGCAACAAAGAGGCCAAGGAGGCGGAGCTCGAGGCCGAGCTGGAGCTGGAGGAGA 5581
Qy 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1895
Db TGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGCAGCCCTTCTCTGTGGCCCGGG 5641
Qy 1895 alGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisI 1915
Db TGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGTCCACACACCACTGCCACACA 5701
Qy 1915 leGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluV 1935
Db TTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCAAGATGGTACCCCAACCCGAGGAGG 5761
Qy 1935 alProValProLeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrH 1955
Db TGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGC 5821
Qy 1955 isSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuG 1975
Db ACTCTCTGCCCAATGACAGCTACATGTGCCGAATGGGACACTGCTGAGAGATCCCTAG 5881
Qy 1975 lyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG 1995
Db GACACAGGGCTGGGGCTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCC 5941
Qy 1995 lnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnP 2015
Db AACCAGCAGACACCAGCTGCATCTACAGCTTCCCAAGATGTGCACTATCTGCTCCAGC 6001

Qy 2015 roHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProL 2035
Db CTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTAACCCACCTGGCCGCTCCCTC 6061
Qy 2035 euAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG 2055
Db TGGCTCAGAGGCCTCTCAGGGCCAGGCAGCAATAAGACTGACTCCCTGGATGTGCAGG 6121
Qy 2055 lyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrA 2075
Db GCCTGGGTAGCCGGAAGACTGTTGTTCAGAGGTGAGTGGGCCCTCTCTGCCCTTGACCC 6181
Qy 2075 rgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnS 2095
Db GGTCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGA 6241
Qy 2095 erLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpA 2115
Db GCAAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGCCAGGCCTGGAAACCAGCTGGG 6301
Qy 2115 laLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIles 2135
Db CCAAGGACCTCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATT 6361
Qy 2135 erGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysC 2155
Db CAGGAGACCTCTTCCAGAGCCAGGAGAAACCCCTGTTCCACGGGACCTGAAGAACT 6421
Qy 2155 ysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnA 2175
Db GCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGGTTCTGGCTAGATGAACAGC 6481
Qy 2175 rgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProS 2195
Db GGAGACACTCCATTGCTGTAGCTGTCTGGACAGCGCTCCCAACCCCGCCTATGTCCA 6541
Qy 2195 erProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysL 2215
Db GCCCTCAAGCCTCGGGGGCAACCTCTTGGGGTCTCTGGAGCCGGCTTAAGAAAAAAC 6601
Qy 2215 euSerProSerIleSerIleAspProProGluSerGlnGlySerArgProProCysS 2235
Db TCAGCCACCCAGTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCA 6661
Qy 2235 erProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerVals 2255
Db GTCCTGGTGTCTGCCCTCAGGAGGGCGCGCCGCCAGTACTCTAAGGATCCCTCGGTCT 6721
Qy 2255 erSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuS 2275
Db CCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTGAGTCTCT 6781
Qy 2275 erGlyLeuSerSerAspProThrAspMetAspPro 2286
Db CTGGTTGTCTTCTGACCAACAGACATGGACCCC 6816
RESULT 6
AAx83486
ID AAx83486 standard; cDNA; 6795 BP.
XX
AC AAx83486;
XX
DT 07-DEC-1999 (first entry)
XX
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Rattus sp.
XX
PN WO9929847-A1.
XX

PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
XX WPI; 1999-394972/33.
DR P-PSDB; AAY14591.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 76-85; 138pp; English.
XX
CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCav1b. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6795
Score: 11751.50 Matches: 2244
Percent Similarity: 99.07% Conservative: 1
Best Local Similarity: 99.03% Mismatches: 8
Query Match: 97.70% Indels: 13
DB: 2 Gaps: 1

US-09-611-257A-24 (1-2287) x AAX83486 (1-6795)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGGATGGAGCGGCGCGGAGGATCGGACAGCCCCGTAGCTTACGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
Db 62 AGCTCAACGACTGTCCGGGCGCGGGCGCGGAGGCGGGGTCGACGGGAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCGCGCGCTAGCCCCGGTGT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAAACC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CGTGGTTCGAGCGAGTCAGTATGTGTGTCATTTCTTCACTGTGTGACTCTGGGTATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCAGGCCGTGTGAGGACATTGCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTCG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTGCCCTTCTTTGCTGTGGAATGGTGGTGAAGATGGTGGCCTTGGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTTCAGCTTCTCCGAGTCAGGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCGACCCCTCAGGGCCATTAAACGGGGTCCCGAGCATGGCATTTCTCG 601
QY 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuCysPhePheV 253
Db 602 TCACATTACTGCTGGACACCTTGCTATGCTGGCAACGTCTCTGCTGCTGCTTCTTCTCG 661
QY 253 alpPheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTTTTCATCTTTGGCATCTGGGCGTCCAGCTGTGGGCGAGACTGCTTTCGCAACCGGT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCTCTCCCGAGAACTTCAGCTCCCTGAGCGTGGACCTGGAGCCTTATTACCAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGAGAT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGGAGTGTGCCACACTGCGTGGGAAGCGGCTGGTGGCCACCCCTGCGAGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrT 353
Db 902 ACTATGAGACCTATAACAGTTCACCAACACCACCTGTGTCAACTGGAACCACTACTATA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyIleAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCTGCGGGCGGAGACAAACCCCTTCAAAGGGCGCCATCAACTTTGACAACTTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCCTGGATCGCCATCTTCCAGGTATCACACTGAGGGCTGGTGGTGGTGGTGGT 1081
QY 393 YrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTCGTAATGGAGCTCACTCTCTTCTTACAACTTCACTACTTCTTCTCATCTCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAAACAGCGGGAGAGTCAGCTGATGCGGAGCAGCGTGTACGATTCCTGTCCAAATGCTA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGGCAAGCTTCTCTGAGCCAGGCTGCTATGAGGAGTACTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTCCGAAAGCAGCCCGAGGGTGGCCAGGTCTCTAGGGCTATAGGCGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
Db 1382 GGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCGAGGAGCCCGCAGCCAGTGGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCACTCGCTCACACCGTGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCACC 1501

QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ACCATCACCACACTACCACCTGGGTAAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGGATGCCAATGGGTCTCGCGGCTCATGTACCACCACCCCTCTACACCCA 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CTCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGACT 1681
QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTGGAGCCAGTCCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCTG 1741
QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
Db 1802 TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CGGGAGCCTGCCATAGCTCCTGCAAAAATCTCCAGCCCTTGCTCCAAGGCACAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGCGGCGCGACAGTTGTCCCTACTGTGCCCCGACAGGAGCAGGAGCCAGATCCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CTGACCATGTATGCCTGACTCAGACAGCGAGGCTGTATGAGTTCAACAGGACGCTC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGTGAACCTCCGGGATCCCCACAGCGCGGCGACAGCGGAGCCTGGGCCCAGATG 2161
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2162 CAGAGCCTAGTTCTGTGTGGCTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATCG 2221
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2222 TAGATAGCAAAATACTTTGGCCGGGAATCATGATCGCCATCTCTGGTCAATACACTCAGCA 2281
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2282 TGGGCATCGAGTACCACGAGCAGCCGAGGAGCTCACCAAGCCCTGGAAATCAGCAACA 2341
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProp 833
Db 2342 TCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGTGAAACTGCTTGTCTACGGTCCCT 2401
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2402 TTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCAATTGTGGTCACTAGTGTGT 2461
QY 853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2462 GGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGTGTGCGGACCTTCCGCTGATGC 2521
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2522 GGGTGTGAAGCTGGTGGCTTCTTCCCGGCCCTGACGGCCAGCTCGTGGTGTCTCATGA 2581

QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhePheS 913
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QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
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QY 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
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QY 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
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QY 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
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QY 993 alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
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QY 1093 luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
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QY 1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
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Db 3722 AGTCAAGGTTTCGTCTCTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTGG 3781
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Db 3782 TCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGACC 3841
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Qy 1573 rgLeuGluLysLysArgArg- 1582
Db 4622 GGCTGGAGAAAAGAGAAGGAATCTAATGTTGGACGATGTAATGCTTCCGGCAGCTCAG 4681
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Db 4802 GGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGACGAGG 4861
Qy 1642 laLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysL 1662
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Qy 1662 euValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaI 1682
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Qy 1842 euValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaL 1862
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Db 5522 AGGAGGAGGCGGAGCTCGAGGCGGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCCGACG 5581
Qy 1882 roHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrA 1902
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Qy 1902 spSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheS 1922
Db 5642 ACAGCCCTAAGCCTGGGGTCCACACACCACTGCCACATTTGAGCAGCCTCGGGCTTCT 5701
Qy 1922 erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA 1942
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Qy 1942 spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT 1962
Db 5762 ACCTGCTGACTGTGAGGAAGTCTGGTGTAGCCGGACGCACTCTCTGCCCAATGACAGCT 5821
Qy 1962 yrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeup 1982
Db 5822 ACATGTCCGCAATGGGAGCACTGTGAGAGATCCCTAGGACACAGGGGTGGGGGTCC 5881

Db	1322	TGTACATCCTCCGAAAGACGAGCCCGAAGGCTGGCCCGAGTCTTAGGGCTATAGGCGTGC	1381
Qy	493	rgAlaGlyLeuLeuSerSerProValAlaAargSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGCTGCTCAGCAGCCCGAGTGGCCCGTAGTGGGCAGGAGCCCAGCCAGTGGA	1441
Qy	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
Db	1442	GCTGCACTCGCTCACACCGTCTGTCTGTCTCCACCACCTGGTCCACCACCATCACCA	1501
Qy	533	isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ACCATCACCACTACCACTGGGTAAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGA	1561
Qy	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT	573
Db	1562	TCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTACCAACCCCTCTACACCCA	1621
Qy	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
Db	1622	CTCCCTCTGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCTACCATGCTGACT	1681
Qy	593	ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
Db	1682	GCCACTTGGAGCCAGTCCGTGTCAGGACCCCTCCAGATGCCCATCGGAGGCATCTG	1741
Qy	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI	633
Db	1742	GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCTGTGTGCATACCAAGCTTCCACCAGAGA	1801
Qy	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS	653
Db	1802	TACTGAAGGATAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACCA	1861
Qy	653	erPheAsnIleProProGlyProPheSerSerMethHisLysLeuLeuGluThrGlnSerT	673
Db	1862	GCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCTCTGGAGACAGAGTA	1921
Qy	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CGGGAGCCTGCCATAGTCTCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAG	1981
Qy	693	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera	713
Db	1982	CCTGCGGGCCGGACAGTTGTCTCTACTGTGCCCCGACAGGAGCAGGAGCCAGAGTCCG	2041
Qy	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
Db	2042	CTGACCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2101
Qy	733	lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGTACCTCCGGGATCCCCACAGCCGGGGGACAGCGGAGCCTGGGCCAGATG	2161
Qy	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
Db	2162	CAGAGCCTAGTTCTGTGCTGGCTTTCTGAGGCTGATCTGTGACACATTCGGGAAGATCG	2221
Qy	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
Db	2222	TAGATAGCAAAATACCTTGGCCGGGGAATCATGATGCCCATCTCTGGTCAATACACTCAGCA	2281
Qy	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2282	TGGGCATCGAGTACACAGCAGCCCGAGGAGTCAACAAAGCCCTGGAAATCAGCAACA	2341
Qy	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2342	TCGTCTTCCACAGCCTCTTCGCTTGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2401
Qy	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2402	TTGGCTACATTAGAAATCCCTACAAACATCTTTGATGGTGTCTATTGCTGCTGCTGCTGCTG	2461

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QY 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4322 GGGTCCGGCACAAAGTACAACCTTTGACAACTTGGGCCAGGCTCTGATGTCCCTGTTGTGC 4381
QY 1493 euAlaSerLysAspGlyTirPValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db 4382 TGGCCTCCAAGGATGGTTGGGTGACATCATGTATGATGGGCTGGATGCTGTGGGTGG 4441
QY 1513 spGlnGlnProIleMetAsnHisAsnProTirPmetLeuLeuTyrPheIleSerPheLeuL 1533
Db 4442 ATCAGCAGCCCATCATGAACCAACCCCTGGATGCTGTATACTTCACTCTCCTCCTCCTCC 4501
QY 1533 euIleValAlaPhePheValIleuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4502 TCATCGTGGCCTTCTTTGTCTCTGAACATGTTTGTGGGCGTGGTGGAGAACTTCCATA 4561
QY 1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
Db 4562 AGTGACACAGCACCCAGGAGGAGGAGCGGAGCGGTGAGGAGAAAGCGACTACGGA 4621
QY 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProT 1593

Db	1662	GGCTGGAGAAAGAGAAGG-----AAAGCCCAAGTGAAGCCCT	4660
Qy	1593	yrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL	1613
Db	4661	ACTACTCTGACTACTCGAGATTCCGGCTCTTGTCACCACTGTGTACCAAGCCACTACC	4720
Qy	1613	euAspLeuPheIleThrGlyValIleGlyLeuAsnValThrMetAlaMetGluHist	1633
Db	4721	TGGACCTCTTTCATCTACTGTTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATT	4780
Qy	1633	yrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI	1653
Db	4781	ACCAGACGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCA	4840
Qy	1653	lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA	1673
Db	4841	TCCTTTGTCTTTGAGTCAGTTTCAAACCTTGGCCCTTTGGCTTCGCCCGTTTCTTCCAGG	4900
Qy	1673	spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG	1693
Db	4901	ACAGGTGGAACACGACTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGG	4960
Qy	1693	luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV	1713
Db	4961	AGGAGATTGAGGTCAATCTGTCTGCTGCCCATCAACCCACCATCATCCGTATCATGAGGG	5020
Qy	1713	alLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL	1733
Db	5021	TGCTCCGCATTGCTCGAGTTCTGAAGTCTGTTGAAGATGGCTGTGGGCATCGGGCCTGC	5080
Qy	1733	euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL	1753
Db	5081	TGCACACGGTGATGCAGGCCCTTGCCCGAGGTGGGAACCTGGGACTTCTCTTCATGTTAT	5140
Qy	1753	euPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT	1773
Db	5141	TGTTTTTTCATCTTTGCAGCTCTGGGCTGGAGCTCTTTGGAGACCTTGGAGTGTGATGAGA	5200
Qy	1773	hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL	1793
Db	5201	CACACCCCTTGTGAGGGCTTGGGTGGGTCGAGCTGCCACCTTTAGGAACCTTTGGTATGGCCCTTC	5260
Qy	1793	euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA	1813
Db	5261	TGACCCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCC	5320
Qy	1813	rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS	1833
Db	5321	GGGACTGTGACCAAGGAGTCCACCTGCTACAAACACTGTATCTCCCTATCTACTTTGTGT	5380
Qy	1833	erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH	1853
Db	5381	CCTTCGTGCTGACCGGCCAGTTTGTGCTGGTCAACGTGGTCAAGTGTGCTGATGAAGC	5440
Qy	1853	isLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluL	1873
Db	5441	ACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGCGGAGCTCGAGGCCGAGCTGGAGC	5500
Qy	1873	euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP	1893
Db	5501	TGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGGAGCCCTTCTCTCTGCG	5560
Qy	1893	roGlyValGluGlyValAsnSerThrAspSerProLysProGlyValAlaProHisThrA	1913
Db	5561	CCGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTG	5620
Qy	1913	laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG	1933
Db	5621	CCCACATTGGAGCAGCCTCGGCTTCTCCCTTGAGACCCCAACGATGGTACCCCAACCCG	5680
Qy	1933	luGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerA	1953
Db	5681	AGGAGGTGCCAGTCCCCCTTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTACGCC	5740
Qy	1953	rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS	1973
Db	5741	GGAGCAGCTCTCTGCCCAATGACAGCTACATGTGCCGAATGGGAGCACTGCTGAGAGAT	5800
Qy	1973	erLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH	1993
Db	5801	CCCTAGGACACAGGGGCTGGGGCTCCCCAAAGCCCACTCAGGCTCCATCTTGTCCGTTTC	5860
Qy	1993	isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL	2013
Db	5861	ACTCCCAACCAAGCAGACACCACTGCTCTTACAGCTTCCCAAGATGTGCACTATCTGC	5920
Qy	2013	euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgS	2033
Db	5921	TCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCACTGGCCGCT	5980
Qy	2033	erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV	2053
Db	5981	CCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGAGCAATAAGGACTGACTCCCTGGATG	6040
Qy	2053	alGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL	2073
Db	6041	TGCAGGGCTGGGTAGCCGGGAAGACCTGTTGTTCAGAGGTGAGTGGGCCCTCTCTGCCCTC	6100
Qy	2073	euThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI	2093
Db	6101	TGACCCGCTCTCATCTTCTGGGGCGGGTTCGAGCATCCAGGTGCAGCAGCGTTCCGGCA	6160
Qy	2093	leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS	2113
Db	6161	TCCAGAGCAAGTCTCCAAGCACATCCGCCCTGCCAGCCCTTGCCAGGCCCTGGAAACCCA	6220
Qy	2113	erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT	2133
Db	6221	GCTGGGCCAAGGACCTCCAGAGACCAGAAAGCAGCTTAGAGCTGGACACGGAGCTGAGCT	6280
Qy	2133	rpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL	2153
Db	6281	GGATTTTCCAGGAGACCTCTTCCAGCAGCCAGGAAGAACCCCTGTTCACCGGACCTGA	6340
Qy	2153	ysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspG	2173
Db	6341	AGAAAGTGTACAGTGTAGAGACCCAGAGCTGCAGGGCGCAGGCTGGGTTCCTGGCTAGATG	6400
Qy	2173	luGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuC	2193
Db	6401	AACAGCGGAGACACTCCATTTGCTGCTGCTGAGCAGCGGCTCCCAACCCCGCCTAT	6460
Qy	2193	ysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysL	2213
Db	6461	GTCCAAGCCCTCAAGCCTCGGGGGCCAACTCTTGGGGTCTCTGGAGCCGGCCTAAGA	6520
Qy	2213	ysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProp	2233
Db	6521	AAAAACTCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCC	6580
Qy	2233	roCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProS	2253
Db	6581	CATGCAGTCTGGTGTCTGCTCAGGAGGAGGCGCGCCAGTACTTAAGGATCCCT	6640
Qy	2253	erValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuS	2273
Db	6641	CGGTCTCCAGCCCCCTTGACAGCACGGTGCCTTACCCCTCCCCAAAGAAAGACACGCTGA	6700
Qy	2273	erLeuSerGlyLeuSerSerAspProThrAspMetAspPro	2286
Db	6701	GTCTCTCTGGTTTGTCTTCTGACCCCAACAGACATGGACCCCC	6741

RESULT: 8
AAD04756
ID AAD04756 standard; cDNA; 7741 BP.

1331 TCTGCTCCAGCCAGCGAGAACGGCATGCGGTCTCTGCAGAAAGCGTGCCACCGCTGGCGG 1390
QY
322 yGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSera 342
Db
1391 GGGACGGGGCGGTGGCCCCACCTTTCGGGTCTGGACTATGAGGCCTACAACAGCTCCAGCA 1450
QY
342 snThrThrCysValAsnTrpAsnGlnTyrThrAsnCysSerAlaGlyGluHisAsnP 362
Db
1451 ACACCACCTGTGCAACTGGAACCACTACTACACCAACTGCTCAGCGGGGAGACAACC 1510
QY
362 roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV 382
Db
1511 CCTTCAAGGGCGCCATCAACTTTGACAACATTGGCTATGCCTGGATCGCCATCTTCCAGG 1570
QY
382 alIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT 402
Db
1571 TCATCACGCTGGAGGGCTGGGTCGACATCATGTACTTTGTGATGGATGCTCATTCCTTCT 1630
QY
402 yrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC 422
Db
1631 ACAATTTCACTACTTCACTCTCTCATCATCGTGGGTCTCTTCTTCATGATCAACCTGT 1690
QY
422 ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA 442
Db
1691 GCCTGGTGGTGATTGCCACGCAGTTCTCAGACCAAGCAGCGGGAAGCCAGCTGATGC 1750
QY
442 rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG 462
Db
1751 GGGAGCAGCGGTGTGCGGTTCTGTCCAACGCCAGCACCTTGGCTAGCTTCTCTGAGCCCCG 1810
QY
462 lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA 482
Db
1811 GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGGTGTACATCCTTCGTAAGGCAGCCCCGCA 1870
QY
482 rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA 502
Db
1871 GGCTGGCTCAGGTCTCTCGGCAGCAGGTGTGCGGTTGGGTGGCTGCTCAGCAGCCCCAGCAC 1930
QY
502 laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeus 522
Db
1931 CCCTCGGGGGCCAGGAGACCCAGCCAGCAGCAGTGTCTCGCTCCACCGCCGCTAT 1990
QY
522 erValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuGlyAsnG 542
Db
1991 CCGTCCACCACCTGGTGACCAACCACCAACCACCATCACCACTACCACTGGGCAATG 2050
QY
542 lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA 562
Db
2051 GGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGACAGGATGCCAATGGGTCCC 2110
QY
562 rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA 582
Db
2111 GCAGGCTCATGCTGCCACCAACCCTCGACGCCTGCCCTCTCCGGGGCCCCCTGGTGGCG 2170
QY
582 laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA 602
Db
2171 CAGAGTCTGTGCACAGCTTCTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG 2230
QY
602 laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT 622
Db
2231 CGCCCCCTCCAGGTCCCCATCTGAGGCATCCGGCAGGACTGTGGGCAGCGGGAAGGTGT 2290
QY
622 yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV 642
Db
2291 ATCCCAACGTCACACACAGCCCTCCACCGGAGACGCTGAAGGAGAAGGCACTAGTAGAGG 2350
QY
642 alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyPropheS 662
Db
2351 TGGCTGCCAGCTTGGGGCCCCCAACCTCACAGCCTCAACATCCACCCCGGCCCTACA 2410
QY
662 erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI 682

Db
2411 GCTCCATGCACAAGCTGCTGGAGACACAGAGTACAGGTGCCTGCCAAAGCTCTTGTCAAGA 2470
QY
682 leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC 702
Db
2471 TCTCCAGCCCTTGTGTTGAAAGCAGACAGTGGAGCCTGTGTCCAGACAGCTGCCCTACT 2530
QY
702 ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps 722
Db
2531 GTGCCCGGGCCGGGCGAGGGAGGTGGAGCTCGCCGACCGTGAAATGCCTGACTCAGACA 2590
QY
722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS 742
Db
2591 GCGAGGCAGTTTATGAGTTCACACAGGATGCCACGACAGCAGCCTCCGGGACCCCCACA 2650
QY
742 erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db
2651 GC---CGGCGGCAACGGAGCCTGGGCCAGATGCAGAGCCCAGCTCTGTGCTGGCCTTCT 2707
QY
762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db
2708 GGAGGCTAATCTGTGACACCTTCGAAAGATTGTGGACAGCAAGTACTTTTGGCCGGGAA 2767
QY
782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db
2768 TCATGATCGCCATCTGTTCAACACACTCAGCATGGGCATCGAATACCACGAGCAGCCCG 2827
QY
802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db
2828 AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTACCAGCCTCTTTGGCCCTGG 2887
QY
822 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db
2888 AGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTTGGGTACATCAAGAAATCCCTACACA 2947
QY
842 lePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnGlyGlyG 862
Db
2948 TCTTCGATGGTGTCTATTGTGTCATCAGCGTGTGGAGATCGTGGGCCAGCAGGGGGGCG 3007
QY
862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
Db
3008 GCCTGTGCTGCTGCGGACCTTCCGCTGTATGCGTGTGTAAGCTGGTGGCTTCTTCTGTC 3067
QY
882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db
3068 CGGCGCTGCAGCGCAGCTGGTGGTGTCTCATGAAGACCATGGACAACGTGGCCACCTTCT 3127
QY
902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db
3128 GCATGCTGCTTATGCTCTTCATCTTTCATCTTTCAGCATCTTGGGCATCTTGGGCATCT 3187
QY
922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db
3188 GCAAGTTTGCCTCTGAGCGGGATGGGGACACCTTGCAGACCCGGAAGAAATTTTGACTCCT 3247
QY
942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962
Db
3248 TGCTCTGGGCCATCGTCACTGTCTTTTCAGATCTTGACCCAGGAGACTGGAAACAAAGTCC 3307
QY
962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
Db
3308 TCTACAAATGGTATGGCCTCCACGTCTTCTGGGGGGCCCCCTTTTATTTTCATTTGCCCTCATGA 3367
QY
982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db
3368 CCTTCGGCAACTACGTCTCTTCAATTTGCTGGTGCCTATCTTGTGGAGGGCTTCCAGG 3427
QY
1002 laGlu----- 1003
Db
3428 CGGAGGAAATCAGCAACCGGGAAGATGCGAGTGGACAGTTAAGCTGTATTTCAGCTGCCTG 3487
QY
1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db
3488 TCGACTCCCGGGGAGATGCCAACAAGTCCGAATCAGAGCCCGATTCTTCTCACCACA 3547

Db 5705 CCCTGCCCCAGGTGGGAACCTGGGACTTCTCTCATGTTGTGTTTTCATCTTTGCAG 5764
QY 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5765 CTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTACGAGACACACCCCTGTGAGGGCC 5824
QY 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals 1799
Db 5825 TGGGCGCTCATGCCACCTTTCGGAACCTTTGGCATGGCCCTTCCTAACCCCTCTTCCGAGTCT 5884
QY 1799 erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5885 CCACAGGTGACAAATTGGAATGGCATTATGAAGGACACCCCTCCGGGACTGTGACCAAGAGT 5944
QY 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5945 CCACCTGCTACAAACACGCTCATCTCGCCTATCTACTTTGTGTCTCTGCTGACGGGCC 6004
QY 1839 lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
Db 6005 AGTTCGTCTAGTCAACCTGGTGATCGCCGCTGTGATGAAGCACCTGGAGGAGAGCAACA 6064
QY 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeus 1879
Db 6065 AGGAGCCCAAGGAGGCGGAGCTAGAGGCTGAGCTGGAGCTGGAGTGAAGACCCCTCA 6124
QY 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
Db 6125 GCCCCAGCCCCCACTCGCCACTGGGCAGCCCCCTCTCTGGCCTGGGTCGAGGGCCCCG 6184
QY 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
Db 6185 ACAGCCCGACAGCCCCCAAGCCTGGGGCTCTGACCCAGCGGCCACCGAGATCAGCCT 6244
QY 1919 erGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProL 1939
Db 6245 CCCACTTTTCCCTGGAGCACCCACGATGACGCCACCCACCCACCGAGCTGCCA----- 6297
QY 1939 euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA 1959
Db 6298 --GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAAGCGCCGACCGACTCTCTGCCCA 6355
QY 1959 snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979
Db 6356 ATGACAGCTACATGTGTCGGCATGGGAGCACTGCCAGGGGCCCTTGGGACACAGGGGCT 6415
QY 1979 rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspt 1999
Db 6416 GGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTCTGTGTCGTTCACTCCCGAGCAGAGATA 6475
QY 1999 hrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlap 2019
Db 6476 CCAGCTACATCTCTGCAGCTTCCCAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCC 6535
QY 2019 roThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgp 2039
Db 6536 CAACCTGGGGCACCATCCCCAACTGGCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGC 6595
QY 2039 roLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySera 2059
Db 6596 CACTCAGGCGCAGGCAGCAATAAGGACTGACTCTTTGGAGCTTCAGGGTCTGGGCAGCC 6655
QY 2059 rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerP 2079
Db 6656 GGGGAAGACCTGTGGCAGAGGTGAGTGGGCCCTTCCCCCGCCCTGGCCCCGGGCTACTCTT 6715
QY 2079 heTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL 2099
Db 6716 TCTGGGGCCAGTCAAGTACCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCA 6775
QY 2099 ysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp 2119

Db 6776 AGCACAATGACCCCGCAGCCCTTGTCCAGGGCCAGAACCCAACTGGGGCAAGGGCCCTC 6835
QY 2119 roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL 2139
Db 6836 CAGAGACCAGAAGCAGCTTAGAGTTGGACACGAGCTGAGCTGAGTGAATTCAGGAGACTCC 6895
QY 2139 eu---ProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerV 2158
Db 6896 TGCCCCCTGGCGCCAGGAGGAGCCCCCATCCCCACGGGACCTGAAGAAGTGTACAGCG 6955
QY 2158 alGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHiss 2178
Db 6956 TGGAGGCCAGAGCTGCCAGGCCCGCCCTACGTCTCTGGTGGATGAGCAGAGGAGACT 7015
QY 2178 erIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSers 2198
Db 7016 CTATCGCGCTCAGCTGCCTGGACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTA 7075
QY 2198 erLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProp 2218
Db 7076 ACCTTGGGGCCAGCCTCTTGGGGGGGCCCGGAGCCCGCCCAAGAAAAAACTCAGCCCCG 7135
QY 2218 roSerIleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyV 2238
Db 7136 CTAGTATCACCATAGACCCCGGAGAGCCCAAGTCTCGGACCCCGCCAGCCCTGGTA 7195
QY 2238 alCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProL 2258
Db 7196 TCTGCCTCCGAGGAGGGTCCCTCCAGCGACTCCCAAGATCCCTTGGCCTCTGGCCCCC 7255
QY 2258 euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeus 2278
Db 7256 CTGACAGCATGGCTGCCTCGCCCTCCCCAAAGAAAGATGTGTGAGTCTCTCCGTTTAT 7315
QY 2278 erSerAspProThrAspMetAspPro 2286
Db 7316 CCTCTGACCCACGACACCTGGACCCC 7341

RESULT 9

AAx83481

ID AAX83481 standard; cDNA; 6750 BP.

XX AC AAX83481;

XX DT 07-DEC-1999 (first entry)

XX DE Human T-type voltage-gated Ca channel alpha-1-G (hCavTla) cDNA.

XX KW Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX OS Homo sapiens.

XX PN WO9929847-A1.

XX PD 17-JUN-1999.

XX PF 30-OCT-1998; 98WO-US023161.

XX PR 05-DEC-1997; 97US-00985809.

XX PA (LOYO) UNIV LOYOLA CHICAGO.

XX PI Perez-Reyes E, Cribbs LL;

XX DR WPI; 1999-394972/33.

XX DR P-PSDB; AAY14586.

XX New T-type voltage-gated calcium channels.

XX PS Disclosure; Page 31-40; 138pp; English.

XX This sequence represents the coding region for a human T-type voltage-

CC gated calcium (Ca) channel alpha-1-G designated hCavTla. Voltage gated
CC channels are membrane bound glycosylated proteins formed of several
CC subunits. The large alpha subunits form a pore in the membrane that is
CC selective for a given ionic species. Each alpha subunit contains 4
CC domains (I, II, III and IV) and each domain contains 6 putative
CC transmembrane helical segments (S1-S6). T-type Ca channels are activated
CC at a lower voltage than L- or N-type channels. Characteristics of T-type
CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel
CC genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc

XX
SQ Sequence 6750 BP; 1290 A; 2170 C; 1984 G; 1306 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6750
Score: 10970.00 Matches: 2111
Percent Similarity: 94.99% Conservative: 32
Best Local Similarity: 93.57% Mismatches: 105
Query Match: 91.20% Indels: 8
DB: 2 Gaps: 4

US-09-611-257A-24 (1-2287) x AAX83481 (1-6750)

QY	34	TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg	53
DB	2	TGGACGAGGAGGAGGATGGAGCGGGCGCGAGGAGTCGGGACAGCCCCGGAGCTTCATGC	61
QY	54	SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGluLysAspp	73
DB	62	GGCTCAACGACCTGTTCGGGGCGGGGGCGGGCGGGCGGGGTTCAGCAAAAGGACC	121
QY	73	roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP	93
DB	122	CGGGCAGCGCGGACTCCGAGGCGAGGGGCTGCCGTACCCGGCGCTGGCCCGGTGTTT	181
QY	93	hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnp	113
DB	182	TCTTCTACTTGAGCCAGGACAGCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAACC	241
QY	113	roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP	133
DB	242	CCTGGTTTGAGCGCATCAGCATGTTGGTCATCCTTCTCAACTGCGTGACCCCTGGGCATGT	301
QY	133	heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA	153
DB	302	TCCGGCCATCGGAGGACATCGCTGTGACTCCAGCGCTGCCGGATCCTGCGGCCCTTTG	361
QY	153	spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI	173
DB	362	ATGACTTCATCTTTCCTTCTTTCCTGCGTGAGATGGTGAAGATGGTGGCCTTGGGCA	421
QY	173	lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI	193
DB	422	TCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA	481
QY	193	leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
DB	482	TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGTTCTCAGCTGTCA	541
QY	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
DB	542	CAGTCCGTGTGTCGACCGCTCAGGGGCCATTAAACCGGGTGCCAGCATCGCATCCTTG	601
QY	233	alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV	253
DB	602	TCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCCTGTCTCTGCTTCTTCG	661

QY	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
DB	662	TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAGGGCTGCTTCGGAACCGAT	721
QY	273	ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
DB	722	GCTTCTACCTGAGAAATTCAGCCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAGA	781
QY	293	hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
DB	782	CAGAAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGGT	841
QY	313	erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA	333
DB	842	CCTGCAGAAAGCGTGCCACGCTGCGGGGACGCGGGCGGTGGCCACCTTGGCGTCTGG	901
QY	333	spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
DB	902	ACTATGAGGCCCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCCAGTACTACA	961
QY	353	hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG	373
DB	962	CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGCCATCAACTTTGACAACATTG	1021
QY	373	lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT	393
DB	1022	GCTATGCCTGGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGCTGGGTGCACATCATGT	1081
QY	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV	413
DB	1082	ACTTTGTGATGGATGCTCATCTCTTACAAATTTTCATCTACTTTCATCTCCTCATCATCG	1141
QY	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
DB	1142	TGGGCTCCTTCTCATGATCAACCTGTGCTGCTGGTGTGATGGCACGCGAGTTCTCAGAGA	1201
QY	433	hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS	453
DB	1202	CCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGTTCTCTGTCAACGCCA	1261
QY	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV	473
DB	1262	GCACCTGGCTAGCTTCTGTAGCCCGGACGCTGTGTATGAGGAGCTGCTCAAGTACCTGG	1321
QY	473	alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493
DB	1322	TGTACATCCTTCGTAAGGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC	1381
QY	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
DB	1382	GGGTGGGCTGCTCAGCAGCCAGCACCCCTTCGGGGGCCAGGAGACCCAGCCAGCAGCA	1441
QY	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
DB	1442	GCTGCTCTCGTCCACCCCGCCCTATCCGTCACACCTGGTGACCCACCACCACCACC	1501
QY	533	isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
DB	1502	ATCACCACTACTACCACTGGGCAATGGACGCTCAGGGCCCCCCCCGGGCCAGCCGGAGA	1561
QY	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT	573
DB	1562	TCCAGGACAGGGATGCCAATGGGTCCCGCCGGCTCATGTGCCACCCCTCGACGCCTG	1621
QY	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
DB	1622	CCCTCTCCGGGGCCCCCTCTGGTGGCGCAGAGTCTGTGCACAGCTTCTTACCATGCCGACT	1681
QY	593	ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
DB	1682	GCCACTTAGAGCCAGTCCCGTGGCCAGGCGCCCCCTCCAGGTTCCCCCATCTGAGGCATCCG	1741

Db 3896 TGGCTGAATGACAGTGAAAGGTGGTGGCACTGGGGCTGGTCTTCGGGGAGCAGGCGTACC 3955

Qy 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373

Db 3956 TCGGAGAGAGTTGGAACGTGTGGACGGGCTGTTGGTGTCTCATCTCCGTATCGACATT 4015

Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393

Db 4016 TGGTGTCCATGGTCTCTGACAGCGGACCAAGATCCTGGGCATGCTGAGGGTGTGCGGC 4075

Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413

Db 4076 TGCTGCGGACCCTGCGCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGTGGTGG 4135

Qy 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlap 1433

Db 4136 TGGAGACGCTGATGTCTCACTGAAACCCATCGGCAACATTGTAGTCATCTGCTGTGCCT 4195

Qy 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453

Db 4196 TCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTGTGCC 4255

Qy 1453 lnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473

Db 4256 AGGCGAGGATACCAGGAACATCAACCAATAATCGGACTGTGCCGAGGCCAGTTACCGGT 4315

Qy 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493

Db 4316 GGGTCCGGCACAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTCGTTT 4375

Qy 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513

Db 4376 TGGCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGTGTGGCGGTGG 4435

Qy 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533

Db 4436 ACCAGAGCCCATCATGAACCAACACCCCTGGATGCTGTGTACTTTCATCTCGTTCCCTGC 4495

Qy 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553

Db 4496 TCATTGTGGCCTCTCTTGTCTGAACATGTTTGTGGGTGGTGGTGAGAGACTTCCACA 4555

Qy 1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgA 1573

Db 4556 AGTGTGCGGAGACACCAGGAGGAAGAGAGGCCCGCGCGGGAGGAGAGCGCCTACGAA 4615

Qy 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProT 1593

Db 4616 GACTGGAGAAAAGAGAGGAGTAAGGAGAGCAGATGGCTGAAGCCCGCAGTGCAGAACCTT 4675

Qy 1593 yrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL 1613

Db 4676 ACTACTCCGACTACTCCCGCTTCGCGCTCCTCGTCCACCACATTGTGCACCAGCCACTACC 4735

Qy 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633

Db 4736 TGGACCTCTTCATCACAGGTGTCTCGGGCTGAACGTGGTCACCATGGCCATGGAGCACT 4795

Qy 1633 yrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1653

Db 4796 ACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGAACATACATCTTCACGTCA 4855

Qy 1653 lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673

Db 4856 TCTTTGTCTGGAGTCAGTTTTCAAACTTGTGGCCCTTGGTTCCGTCCGTTCTTCCAGG 4915

Qy 1673 spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693

Db 4916 ACAGGTGAACACGACTGGACCTGGCCATTGTGCTGTGTGTCCATCATGGGCATCACGCTGG 4975

Qy 1693 luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713

Db 4976 AGGAAATCGAGGTCAACGCCTCGCTGCCCATCAACCCCAACCATCATTCGGCATCATGAGGG 5035

Qy 1713 alLeuArgIleAlaAargValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733

Db 5036 TGCTGCGCATTTGCCGAGTGTCTGAAGCTGCTGAAGATGGCTGTGGCATGCGGGCGCTGC 5095

Qy 1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753

Db 5096 TGGACACGGTGATGCAGGCCCTGCCCCCAGGTGGGAACTTGGGACTTCTCTTTCATGTTGT 5155

Qy 1753 euPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773

Db 5156 TGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGA 5215

Qy 1773 hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793

Db 5216 CACACCCCTGTGAGGGCCTGGGCGCTCATGCCACCTTTTCGGAACCTTTGGCATGGCCTTCC 5275

Qy 1793 euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813

Db 5276 TAACCCCTCTTCCGAGTCTCCACAGGTGACAAATTGGAAATGGCATTATGAAGGACACCCCTCC 5335

Qy 1813 rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleIlePheValS 1833

Db 5336 GGGACTGTGACAGGAGTCCACCTGTCTACAACACGGTTCATCTCGCCTATCTACTTTGTGT 5395

Qy 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853

Db 5396 CCTTCGTGCTGACGGCCAGTTCGTGTCTAGTCAACGTGGTGATCGCCGTGCTGATGAAGC 5455

Qy 1853 isLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluL 1873

Db 5456 ACCTGGAGGAGAGCAACAAGGAGGCCAAGGAGGCGGAGCTAGAGGCTGAGCTGGAGC 5515

Qy 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP 1893

Db 5516 TGGAGATGAAGACCTTCAGCCCCCAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTTGGC 5575

Qy 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913

Db 5576 CTGGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGG 5635

Qy 1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933

Db 5636 CCCACGCGAGATCAGCCTCCCACTTTTCCCTGGAGCACCCACAGATGCAGCCCCACCCCA 5695

Qy 1933 luGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerA 1953

Db 5696 CGGAGCTGCCA-----GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAGCC 5746

Qy 1953 rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS 1973

Db 5747 GAACGCACCTCTCTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGGC 5806

Qy 1973 erLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993

Db 5807 CCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCCTTGTCCGTTT 5866

Qy 1993 isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL 2013

Db 5867 ACTCCAGCCAGCAGATACAGCTACATCTCTGCAGCTTCCCAAAGATGCACCTCATCTGC 5926

Qy 2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgS 2033

Db 5927 TCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCCAACCCAGGACGCT 5986

Qy 2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspv 2053

Db 5987 CCCCTTTGGCTCAGAGGCCACTCAGGGCGCCAGGCAGCAATAAGGACTGACTCTCTTGGACG 6046

Qy 2053 alGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073

Db 6047 TTCAGGGTCTGGGCAGCCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTTCCCCGCCCC 6106

Qy 2073 euThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093
|||:::|||||
Db 6107 TGGCCCGGCCTACTCTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCATCCCGCA 6166

Qy 2093 leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
|||:::|||||
Db 6167 GCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGCCACAGGCCCCAGAACCCA 6226

Qy 2113 erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
:::|||||
Db 6227 ACTGGGGCAAGGCCCTCCAGAGACCAGAACAGCAGCTTAGAGTTGGACACGGAGCTGAGCT 6286

Qy 2133 rpIleSerGlyAspLeuLeu---ProSerSerGlnGluGluProLeuPheProArgAspL 2152
|||:::|||||
Db 6287 GGATTTTCAGGAGACCTCTGCCCCCTGGCGGCAGGAGGAGCCCCCATCCCCACGGGACC 6346

Qy 2152 euLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuA 2172
|||:::|||||
Db 6347 TGAAGAAGTGCTACAGCGTGGAGGCCAGAGTGCCAGCGCGGCTACGTCTCGCTGGTGG 6406

Qy 2172 spGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgL 2192
|||:::|||||
Db 6407 ATGACGAGGAGAGACTCTATCGCGTCACTGCTGGACAGCGGCTCCCAACCCACC 6466

Qy 2192 euCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProL 2212
|||:::|||||
Db 6467 TGGGCACAGACCCCTTAACCTTGGGGGCCAGCCTCTTGGGGGGCTGGGAGCGGCCCA 6526

Qy 2212 ysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgP 2232
|||:::|||||
Db 6527 AGAAAAAATCAGCCCCCTAGTATCACCATAGACCCCCCGAGAGCAAGGTCTCTCGGA 6586

Qy 2232 roProCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspP 2252
|||:::|||||
Db 6587 CCCCAGCCAGCCCTGGTATCTGCTCCGAGGAGGCTCCGTCCAGCGACTCCAAGGATC 6646

Qy 2252 roSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrL 2272
|||:::|||||
Db 6647 CCTTGGCCTCTGGCCCCCTTGACAGCATGGCTGCCTCGCCCTCCCCCAAGAAAGATGTGC 6706

Qy 2272 euSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
|||:::|||||
Db 6707 TGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACTGGACCCC 6750

RESULT 10
AAX83483
ID AAX83483 standard; cDNA; 6804 BP.
XX AAX83483;
AC AAX83483;
XX 07-DEC-1999 (first entry)
DT
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c) cDNA.
DE
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX Homo sapiens.
OS
XX WO9929847-A1.
PN
XX 17-JUN-1999.
PD
XX 30-OCT-1998; 98WO-US023161.
PF
XX 05-DEC-1997; 97US-00985809.
PR
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX Perez-Reyes E, Cribbs LL;
PI
XX WPI; 1999-394972/33.
DR P-PSDB; AAY14588.

XX New T-type voltage-gated calcium channels.
PT
XX Disclosure; Page 49-58; 138pp; English.
PS

XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6804 BP; 1301 A; 2186 C; 1998 G; 1319 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6804
Score: 10946.00 Matches: 2110
Percent Similarity: 94.20% Conservative: 32
Best Local Similarity: 92.79% Mismatches: 106
Query Match: 91.00% Indels: 26
DB: 2 Gaps: 5

US-09-611-257A-24 (1-2287) x AAX83483 (1-6804)

Qy 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
|||:::|||||
Db 2 TGGACGAGGAGGAGGATGGAGCGGGCGCGGAGGATCGGGACAGCCCCCGGAGCTTCATGC 61

Qy 54 SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGluLysAspP 73
|||:::|||||
Db 62 GGCTCAACGACCTGTTCGGGGCGCGGGGGCGCGGGGGTTCAGCAGAAAGGACC 121

Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
|||:::|||||
Db 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCGGTGTTT 181

Qy 93 hepTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
|||:::|||||
Db 182 TCTTCTACTTGAGCAGGACAGCCCGCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAAC 241

Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
|||:::|||||
Db 242 CCTGGTTTGAGCGCATCAGCATGTTGGTTCATCCTTCTCAACTGGGTGACCCCTGGGCATGT 301

Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
|||:::|||||
Db 302 TCCGGCCATCGGAGACATCGCCTGTGACTCCAGCGCTCCCGGATCCTGCAGGCCCTTG 361

Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
|||:::|||||
Db 362 ATGACTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGCA 421

Qy 173 lepPheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
|||:::|||||
Db 422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGGCTTGACTTTTCATCGTCA 481

Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
|||:::|||||
Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACCTGACGCTTCTCAGCTGTTCAGGA 541

Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCCGTGTGCTCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATCGCATCCTTG 601
QY 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCCTGCTGTCTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGGCTCCAGCTGTGGCAGGGCTGCTTCGGAACCGAT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTACCTGAGAAATTTACGCCTCCCTTGAGCGTGGACCTGGAGCGCTATTACCAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCGCACGCGAGAACGGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAACGCTGCCACGCTGCGGGGACGGGGCGGTGGCCACCTTGCGGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGCGCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGGCATCAACTTTGACAAACATTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCCTGGATCGCCATCTTCCAGGTCAACGCTGGAGGGCTGGTCCGACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTTGTGTGATGTCTCATTCCTTCTACAAATTTTCATCTACTTTCATCCTCCTCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTCATGTATCAACCTGTGCCTGGTGTGATTGCCACGCAGTTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas 453
Db 1202 CCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTGATTGCCACGCAGTTC 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCCCTGGTAGCTTCTCTGAGCCGGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCGCAGCACCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACCTGGTGCACCACCACCACCACC 1501
QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACCACTACCACCTGGCAATGGGACGCTCAGGGGCCCGGGCCAGCCCGGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACCCTCGACGCCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CCCTCTCGGGGCCCCCCTGTGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCGGACT 1681
QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCCAGGTCCCCCATCTGAGGCATCCG 1741
QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGGACTGTGGCAGCGGGGAAGGTGTATCCCACCGTGCACACCAGCCCTCCACCCGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValAlaAlaProSerProGlyProProThrLeuThrS 653
Db 1802 CGCTGAAGGAGAAGGCACTAGTAGAGGTGGCTGCCAGTCTTGGGCCCCCAACCCCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCCCGGCCCTACAGTCCATGCACAAGCTGCTGGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTGCCAAAGCTCTTGAAGATCTCCAGCCCTGCTTGAAGCAGACAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGCTCCAGACAGCTGCCCTACTGTGCCCGGGCGGGCAGGGAGGTGGAGCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCCGTGAATGCCTGACTCAGACAGCGAGGCAGTTATGAGTTTACACACAGGATGCC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCGACCTCCGGGACCCCCACAGC--CGGCGGCAACGGAGCCTGGGCCCAGATG 2158
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCAGCTCTGTGTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCA 2278
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACGAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
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QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTTCATTGTGGTTCATCAGCGTGT 2458
QY 853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGCGGCCCTGTGCGTGTGCTGCGGACCTTCCGCTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
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QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
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QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
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Db 4916 TCITGGAGTCAGTTTTCAAACTTGTGGCCTTTGGTTTCCTCGGTTCCTCCAGGACAGGT 4975
QY 1675 rpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluI 1695
Db 4976 GGAACCACTGGACCTGGCCATTGTGCTGTCTCCATCATGGGCATCACGCTGGAGGAA 5035
QY 1695 leGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuA 1715
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QY 1715 rgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHist 1735
Db 5096 GCATTGCCGAGTGTGAAGCTGTGAAGATGGCTGTGGGCATCGGGCGCTGTGGACA 5155
QY 1735 hrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
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Db 5216 TCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACTGGAGTGTGACGAGACACACC 5275
QY 1775 roCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
Db 5276 CCTGTGAGGGCCTGGGCCGTGTCACCTTTTCGGAACCTTTGGCATGGCCTTCCTAAACCC 5335
QY 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspC 1815
Db 5336 TCTTCCGAGTCTCCACAGGTGACAATTGGAATGGCAATTATGAAGGACACCCCTCCGGGACT 5395
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QY 1855 luGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLum 1875
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QY 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1895
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QY 1895 alGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisI 1915
Db 5636 TCGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCCTGGGCTCTGCACCCAGCGGCCACG 5695
QY 1915 leGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluV 1935
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QY 1975 lyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG 1995
Db 5867 GACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAGGCTCCGTCTTGTCCGTTCACCTCCC 5926
QY 1995 lnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrIleLeuGlnP 2015
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QY 2015 roHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProProGlyArgSerProL 2035

Db 5987 CCCACAGCGCCCAACCTGGGGCACCATCCCCAAACTGCCCCACCAGGACGCTCCCTT 6046
QY 2035 euAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG 2055
Db 6047 TGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAATAAGACTGACTCCTTGGACGTTTCAGG 6106
QY 2055 lyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrA 2075
Db 6107 GTCTGGGAGCCCGGAAGACCTGTGGCAGAGGTGAGTGGGCCCTCCCGGCCCTGGCCC 6166
QY 2075 rgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnS 2095
Db 6167 GGGCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACA 6226
QY 2095 erLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpA 2115
Db 6227 GCAAGATCTCAAGCACATGACCCCGCCAGCCCTTGTCCAGGCCAGAACCCAACTGGG 6286
QY 2115 laLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIles 2135
Db 6287 GCAAGGGCCCTCCAGAGACCAAGAAGCAGCTTAGAGTTGGACACGGAGCTGAGTGATTT 6346
QY 2135 erGlyAspLeuLeu---ProSerSerGlnGluGluProLeuPheProArgAspLeuLysL 2154
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QY 2154 ysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluG 2174
Db 6407 AGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCTACGTCTCTGGCTGGATGAGC 6466
QY 2174 lnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysP 2194
Db 6467 AGAGGAGACACTCTATCGCGCTCAGCTGCCTGGACAGCGGCTCCCAACCCCACTGGGCA 6526
QY 2194 roSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysL 2214
Db 6527 CAGACCCCTTAACCTTGGGGGCCAGCCTCTTTGGGGGCTGGGAGCGCGCCCAAGAAAA 6586
QY 2214 ysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProProC 2234
Db 6587 AACTCAGCCCGCTAGTATCACCATAGACCCCCCGAGAGCCCAAGGTCTCTCGGACCCCGC 6646
QY 2234 ysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerV 2254
Db 6647 CCAGCCTGGTATCTGCTCTCGGAGGAGGCTCCGTCCAGCGACTCCAAGGATCCCTTGG 6706
QY 2254 alSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerL 2274
Db 6707 CCTCTGGCCCCCTTGACAGCATGGCTGCCTCGCCCTCCCCAAAGAAAGATGTGTGAGTC 6766
QY 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6767 TCTCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 6804
RESULT 11
AAX83482
ID AAX83482 standard; cDNA; 6783 BP.
XX
AC AAX83482;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1b) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN WO9929847-A1.
XX
PD 17-JUN-1999.
XX

PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAY14587.
XX
PT New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 40-49; 138pp; English.
PS
XX
CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX
SQ Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6783
Score: 10923.50 Matches: 2105
Percent Similarity: 94.31% Conservative: 33
Best Local Similarity: 92.85% Mismatches: 110
Query Match: 90.82% Indels: 19
DB: 2 Gaps: 5

US-09-611-257A-24 (1-2287) x AAX83482 (1-6783)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGGATGGAGCGGCGCCGAGAGTCCGGACAGCCCCGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGluLysAspP 73
Db 62 GGCTCAACGACCTGTCCGGGGCGGGGGCGGCGCGGCGCGGGTCCAGCAAAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCGGTGGTTT 181
QY 93 hepheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAGCCAGGACAGCGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAACC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTTGAGCGCATCAGCATGTGGTCATCTCTCAACTGCGTGACCCCTGGGCATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATGCCAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCTCTGCGGCTTTG 361
QY 153 spAspPheIlePheAlaPheAlaValGluMetValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTTCATCTTTCCTTCTTTGCGGTGGAGATGGTGTGAAGATGGTGGCCTTGGGCA 421

QY 173 lepheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAAGTGTATTACCTGGGAGACACTTGGAAACGGCTTGACTTTTTCATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTTCAGCTTCTCAGCTGTCCAGGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTTG 601
QY 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGGATACGCTGCCCATGCTGGCAACGTCTGCTGCTCTGCTTCTTCG 661
QY 253 alpPheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAACCGAT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCTCTACCTGAGAAATTCAGCCCTCCCTGCTGCTGCCAGCGCTGAGCGCTATTACCA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCAGCGAGAACCGGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAAAGCTGCCACGCTGCCGGGGACGGGGGGCGGTGGCCACCTTTCGGGTCTGG 901
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Db 902 ACTATGAGGCTTACAACAGCTCCAGCAACACACACCTGTGTCAACTGGAACCACTACTACA 961
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Db 962 CCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACATTG 1021
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QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
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QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCCTGTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGTGTCTCAAGTACCTGG 1321
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QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCACCGCGCCCTATCCCTCCACACCTGGTGCACCCACCAACCACC 1501

QY 533 isHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
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Db 1562 TCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCAACCTCGACGCCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
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QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCGGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCCG 1741
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Db 1742 GCAGGACTGTGGGCAGCGGGAAAGTGTATCCACCGTGACACACAGCCCTCCACCGGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGGAGAAGGCACCTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCCGGGCCCTACAGCTCCATGCCAACAGTCTGTGGAGACACAGATA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGGAG 1981
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Db 1982 CCTGTGTCCAGACAGCTGCCCTACTGTGCCCGGCGGGGAGGTGGAGTCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAATGCCTGACTCAGACAGCGAGGAGCTTATGAGTTTACACAGGATGCCC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCGACCTCCGGACCCCCACAGC--CGGCGGCAACGGAGCCTGGGCCAGATG 2158
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCAGACTCTGTGTGGCCCTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCTGTTCAACACACTCAGCA 2278
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACGAGCAGCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
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Db 2339 TCGTCTTCACAGCCTCTTTGCCCTGGAGATGCTGCTGAAGTGTCTGTGTATGGTCCCT 2398
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
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Db 3176 AGATGAAGTCAACGCCCAAGCCCGCAGCTCTCCGACAGCCCTGGAGCGCTGCAAGCA 3235
QY 1113 erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
Db 3236 GCTGGACCAGCAGGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAAGCGGA 3295
QY 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGlnAspG 1153
Db 3296 GAAGCCCAAGTGGAGAGCGGGGTCCCTGTTGTTCGGGAGAAGGCCAGGAGAGCAGGATG 3355
QY 1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
Db 3356 AAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTTGGGGCAGTGACCATCGCCACAGGG 3415
QY 1173 lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
Db 3416 GGTCCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCGAGTGCAG 3475
QY 1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
Db 3476 GGTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTTGAGCACACAGGACTGCAATGGCA 3535
QY 1213 ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3536 AGTCGGCTTCAGGGCGCTGCGCCCGGCCCTTGGCGCCTGATGACCCCCACTGGATGGG 3595
QY 1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
Db 3596 ATGACCCCGATGACGAGGGCAACCTGAGCAAAGGGGAACGGGTCCGCGCGTGGATCCGAG 3655
QY 1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
:::|||||

Db 3656 CCCGACTCCCTGCTTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCTCCTC 3715

Qy 1273 InSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293

Db 3716 AGTCCAGGTTCCGCTCCTGTGTACCCGGATCATCACCCACAAGATGTTCCAGCACGTGG 3775

Qy 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspp 1313

Db 3776 TCCTTGTCATCATCTTCTTAACCTGCATCACCATCGCCATGGAGCGCCCAAAATTGACC 3835

Qy 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333

Db 3836 CCACAGCGCTGAACCGCATCTTCTGACCCCTCTCCAATTACATCTTACCCGAGTCTTTC 3895

Qy 1333 euAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrL 1353

Db 3896 TGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCCTTCCGGGAGCAGGCGTACC 3955

Qy 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373

Db 3956 TCGGAGCAGTTGGAACGTGCTGGACGGGCTGTGGTGTCTCATCTCCGTCAATCGACATTC 4015

Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393

Db 4016 TGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTGCGGC 4075

Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413

Db 4076 TGCTGGGACCCCTGCGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTGGTGG 4135

Qy 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaP 1433

Db 4136 TGGAGACGCTGATGTCTCTACTGAAACCCATCGGCAACATTTAGTCACTGTGTCCT 4195

Qy 1433 hepHeIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453

Db 4196 TCITTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTGTGCC 4255

Qy 1453 lnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473

Db 4256 AGGGCGAGATACCAGGAACATACCAATAAATCGGACTGTCCGAGGCCAGTTACCGGT 4315

Qy 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493

Db 4316 GGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTCTGTTT 4375

Qy 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513

Db 4376 TGGCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTGTGGCGGTGG 4435

Qy 1513 spGlnGlnProfileMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533

Db 4436 ACCAGCAGCCCATCATGAACCAACACACCCCTGGATGCTGCTGTACTTTCATCTCGTTCCTGC 4495

Qy 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553

Db 4496 TCATTGTGGCCTTCTTGTCTGAAACATGTTTGTGGTGTGGTGGTGGAGAACTTCCACA 4555

Qy 1553 ysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573

Db 4556 AGTGTGGCAGCACCCAGGAGGAAGAGGAGGCCCGCGGGAGGAGAGCGCCTACGAA 4615

Qy 1573 rgLeuGluLysLysArgArg-----SerLysG 1582

Db 4616 GACTGGAGAAAAGAGAAAGGAATCTAATGCTGGACGATGTAATGCTTCCGGCAGCTCAG 4675

Qy 1582 luLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgL 1602

Db 4676 CCAGCGCTGGTCCAGAAAGCCAGTGCAAAACCTTACTCTCCGACTACTCCCGCTTCCGGC 4735

Qy 1602 euLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleG 1622

Db 4736 TCCTCGTCCACCACTGTGTGCACCAGCCACTACCTGGACCTTTCATCATCACAGGTGTATCG 4795

Qy 1622 lyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluA 1642

Db 4796 GGCTGAACGTGGTCAACCATGGCCATGGAGCATTACCAGCAGCCCCAGATTCTGGATGAGG 4855

Qy 1642 laLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysL 1662

Db 4856 CTCTGAAGATCTGCAACTACATCTTCACTGTCACTTGTCTTGGAGTCAGTTTCAAAC 4915

Qy 1662 euValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaI 1682

Db 4916 TTGTGGCCTTTGGTTTCCGTCCGTCTTCCAGGACAGGTGGAACCCAGCTGGACCTGGCCA 4975

Qy 1682 leValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeup 1702

Db 4976 TTGTGCTGCTGCCATCATGGGCATCACGCTGGAGGAAATCGAGGTCAACGCCCTCGTGC 5035

Qy 1702 roIleAsnProThrIleIleArgIleMetArgValIleuArgIleAlaArgValLeuLysL 1722

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Qy 1722 euLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProG 1742

Db 5096 TGCTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACGGTGATGCAGGCCCTGCCCC 5155

Qy 1742 lnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyV 1762

Db 5156 AGGTGGGGAACCTGGGACTTCTCTCATGTTGTTGTTTTTTCATCTTTTGCAGCTCTGGCG 5215

Qy 1762 alGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgH 1782

Db 5216 TGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCCTGGCGCTC 5275

Qy 1782 isAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyA 1802

Db 5276 ATGCCACCTTTCGGAACCTTTGGCATGGCCTTCTTAACCCCTTCTCCGAGTCTCCACAGTG 5335

Qy 1802 spAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrCyst 1822

Db 5336 ACAATTGGAATGCAATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCACCTGCT 5395

Qy 1822 yrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValL 1842

Db 5396 ACAACACGGTCACTCGCCTATCTACTTGTGTCCTTCGTGCTGACGGCCAGTTCTGTCG 5455

Qy 1842 euValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaL 1862

Db 5456 TAGTCAACGTGGTATGCGCGTGTGTATGAAGCACCTGGAGGAGAGCAACAAGAGGCCA 5515

Qy 1862 ysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnP 1882

Db 5516 AGGAGGAGGCCGAGCTAGAGGTGAGCTGAGCTGGAGATGAAGACCTTCAGCCCCCAGC 5575

Qy 1882 roHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThra 1902

Db 5576 CCCACTCGCCACTGGGCAGCCCTTCCCTTGGCCTGGGTTCGAGGGCCCCCAGCCCCCG 5635

Qy 1902 spSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheS 1922

Db 5636 ACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCCCACCGAGATCAGCTCCACTTTT 5695

Qy 1922 erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA 1942

Db 5696 CCCTGGAGCACCCACGATGCAGCCCCCACCACCCAGGAGCTGCCA-----GGACCAG 5746

Qy 1942 spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT 1962

Db 5747 ACITACTGACTGTGCGGAAGTCTGGGGTCAGCCCAACGCACCTCTCTGCCCAATGACAGCT 5806

Qy 1962 yrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeup 1982

Db 5807 ACATGTGTGGCATGGGAGCACTGCCGAGGGGGCCCCCTGGGACACAGGGGCTGGGGGTCC 5866

Qy	1982	roLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI	2000
Db	5867	CCAAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCAGCCAGCAGATACCAGCTACA	5926
Qy	2002	leLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpG	2022
Db	5927	TCCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCCCAACCTGGG	5986
Qy	2022	lyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgA	2042
Db	5987	GCACCATCCCCAACTGCCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGC	6046
Qy	2042	rgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspL	2062
Db	6047	GCCAGGCAGCAATAAGGACTGACTCCTTGGACGTTTCAGGGTCTGGGCAGCCGGGAAGACC	6106
Qy	2062	euLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyG	2082
Db	6107	TGCTGGCAGAGGTGAGTGGGCCCTCCCCGCCCTTGGCCCCGGGCTACTCTCTTTTGGGGCC	6166
Qy	2082	lySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleA	2102
Db	6167	AGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGA	6226
Qy	2102	rgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrA	2122
Db	6227	CCCCGCCAGCCCCCTTGCCAGGCCCCAGAACCCCACTGGGGCAAGGGCCCCCTCCAGAGACCA	6286
Qy	2122	rgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu--ProS	2141
Db	6287	GAAGCAGCTTAGAGTTGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTCTGCCCTTG	6346
Qy	2141	erSerGlnGluGluProLeuPheProArgAspLeuLysCysTyrSerValGluThrG	2161
Db	6347	GCGGCCAGGAGGAGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGCC	6406
Qy	2161	lnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlav	2181
Db	6407	AGAGCTGCCAGCGCGGCTACGTCTCTGGTGGATGAGCAGAGGAGACACTCTATCGCCG	6466
Qy	2181	alSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyG	2201
Db	6467	TCAGCTGCCTGGACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTAACCTTGGGG	6526
Qy	2201	lyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProProSerIles	2221
Db	6527	GCCAGCCTCTTGGGGGGCCTGGGAGCGGCCCAAGAAAAAACTCAGCCCCCTAGTATCA	6586
Qy	2221	erIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuA	2241
Db	6587	CCATAGACCCCCCGAGAGCCAAAGGTCTCTGGACCCCGCCAGCCCTGGTATCTGCTCTCC	6646
Qy	2241	rgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSerT	2261
Db	6647	GGAGGAGGGCTCCGTCAGCGACTCCAAGGATCCCTTGGCCCTCTGGCCCCCTGACAGCA	6706
Qy	2261	hrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspP	2281
Db	6707	TGGCTGCCTCGCCCTCCCCAAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCTCTGACC	6766
Qy	2281	roThrAspMetAspPro	2286
Db	6767	CAGCAGACCTGGACCCC	6783

RESULT 12
AAX83484

AA83484
ID AAX83484 standard; cDNA; 6729 BP.

XX
AC AAX83484;

DT 07-DEC-1957 XX

Human T-t

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX Homo sapiens.
XX WO9929847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
DR P-PSDB; AAY14589.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 58-67; 138pp; English.
XX
CC This sequence represents the coding region for a human T-type voltage-
CC gated calcium (Ca) channel alpha-1-G designated hCavTld. Voltage gated
CC channels are membrane bound glycosylated proteins formed of several
CC subunits. The large alpha subunits form a pore in the membrane that is
CC selective for a given ionic species. Each alpha subunit contains 4
CC domains (I, II, III and IV) and each domain contains 6 putative
CC transmembrane helical segments (S1-S6). T-type Ca channels are activated
CC at a lower voltage than L- or N-type channels. Characteristics of T-type
CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AX83481-X83492 represent novel T-type voltage-gated Ca channel
CC genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc

Db 242 CCTGGTTTGAGCGCATCAGCATGTTGGTCATCCTTCTCAACTGCGTGACCCCTGGGCATGT 301
Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATCGGAGACATCGCCTGTGACTCCAGCGCTCGCGGATCCTGACGCCCTTG 361
Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTTGGCTTCTTTGCCGTGAGATGGTGGTGAAGATGGTGGCCTTGGCA 421
Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAAGTGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCAAGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTCGACCGCTCAGGGCCATTAAACCGGTGCCAGCATGCGCATCCTTG 601
Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTCTGCTTCTTCG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGAGGGCTGCTTCGGAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCTTACCTGAGATTTACGGCTCCCCCTCAGCTGAGCGTGAGACCTGGAGCGCTATTACCAGA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGCGATGCGGT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAAAGCTGCCACGCTGCGCGGGGACGCGGGGCGGTGGCCCCACCTTGGCGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCCTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTACA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACATTG 1021
Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
Db 1022 GCTATGCTTGGATCGCCATCTTCCAGGTATCAGCTGGAGGSGTGGTGCACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACCTTGTGTGATGGATGCTCATTCCTTCTACAAATTTCATCTACTTCCTCCTCATCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGTGATTGCCAGCGAGTTCTTCAGAGA 1201
Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGTGATCGGGAGCAGCGGTGTGCGGTTCTGTCCAACGCCA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCCCTGGTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
Qy 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493

Db 1322 TGTACATCCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCACGAGCA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCACCCGCGCTATCCGTCCACCACCTGGTGACCAACCACCAACC 1501
Qy 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACCACTACCACTGGCAATGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGA 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGGATGCCAATGGTCCCGCGGCTCATGTGCCACCAACCCTCGACGCTG 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCCTCTCCGGGGCCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681
Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCCCATCTGAGGCATCCG 1741
Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGGACTGTGGCAGCGGGAAGGTGTATCCCAACCGTGCACACCAAGCCCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
Db 1802 CGCTGAAGGAGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCCCTCACA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCCACCCCGGGCCCTACAGCTCCATGCACAAAGCTGTGGAGACACAGAGTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGGAG 1981
Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGTTCCAGACAGCTGCCCTACTGTGCCGGCCCGGGCAGGGGAGGTGGAGCTCG 2041
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAAATGCTGACTCAGACAGCGAGGCGAGTTTATGAGTTCACACAGGATGCCC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCGACCTCCGGGACCCCAACAGC--CGGGCGCAACGGAGCCTGGGCCACAGATG 2158
Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGCAGCAAGTACTTTTGGCCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCA 2278
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACGAGCAGCCCGAGGAGCTTACCAACGCCCTTAGAAATCAGCAACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTACACGAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGGTCCCT 2398
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTCTATTGTGTTCATCAGCGTGT 2458

QY 853 rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGCCAGCAGGGGGGGCGCTGTGCGTGTGCGGACCTTCCGCCGTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGGTGGCTTCCCTGCGGCGCTGCAGCGGAGCTGGTGTGCTCATGA 2578
QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhePheS 913
Db 2579 AGACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTCA 2638
QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCCTGGGATGCATCTCTTCGGCTGCAAGTTTGGCTCTGAGCGGGATGGGGACACCC 2698
QY 933 euProAspArgLysAsnPheAspSerLeuLeuTirAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCCGAAGAATTTTGACTCCTTGCTCTGGGCCATCGTCACTGTCTTTCAGATCC 2758
QY 953 euThrGlnGluAspTirAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTirPA 973
Db 2759 TGACCCAGGAGACTGGAACAAAGTCTCTACAATGGTATGGCCTCCACGTCGTCTGGG 2818
QY 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2819 CGGCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTAGCTGCTCTTCAATTTGCTGG 2878
QY 993 alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
Db 2879 TCGCCATTTCTGGTGAGGGCTTCCAGCGGAGGAGATGCCAACAAAGTCCGAATCAGAGC 2938
QY 1013 roAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV 1033
Db 2939 CCGATTTCTTCTCACCCAGCCTGGATGGTGTATGGGGACAGGAAGTGTCTTGGCCTTGG 2998
QY 1033 alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT 1053
Db 2999 TGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGTGCGCGCTCTCATCATCCACA 3058
QY 1053 hrAlaAlaThrProMetSerHisProLysSerSerSerSerThrGlyValGlyGluAlaLeuG 1073
Db 3059 CGGCCGCCACCCCATGTGCTGCCAAGAGCACACGCGGCTTGGCGGAGCGCTGG 3118
QY 1073 lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisG 1093
Db 3119 GCCCTGCGTCGCGCCGACCCAGCAGCAGCGGGTTCGGCAGAGCCTTGGGCGGCC--CACG 3175
QY 1093 luMetLysCysProProSerAlaArgSerSerProHisSerProTirSerAlaAlaSerS 1113
Db 3176 AGATGAAGTACCCGCCAGCGCCCGCAGCTCTCCGCACAGCCCTTGAGCGCTGCAAGCA 3235
QY 1113 erTirThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
Db 3236 GCTGGACCAAGCGCGCTCCAGCCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGA 3295
QY 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG 1153
Db 3296 GAAGCCCAAGTGGAGAGCGGGCTCCCTGTTGTCGGGAGAAGGCCAGGAGAGCAGGATG 3355
QY 1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
Db 3356 AAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTGCGGCGAGTGACCATCGCCACAGGG 3415
QY 1173 lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
Db 3416 GGTCCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAAGTGCAG 3475
QY 1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
Db 3476 GGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAATGGCA 3535

QY 1213 ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3536 AGTCGGCTTCAGGGCGCCTGGCCGGGCCCTGCGGCCTGATGACCCCCACTGGATGGG 3595
QY 1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTirPValArgS 1253
Db 3596 ATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGTCCGCGCTGGATCCGAG 3655
QY 1253 erArgLeuProAlaCysCysArgGluArgAspSerTirPserAlaTyrIlePheProProG 1273
Db 3656 CCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCTCCTC 3715
QY 1273 lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
Db 3716 AGTCCAGGTTCCGCCCTCCTGTGTACCCGATCATCACCAAGATGTTTCGACCCAGCTGG 3775
QY 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313
Db 3776 TCCTTGTTCATCATCTTCCTTAACTGCATCACCATCGGCATGGAGCGCCCCAAAATTGACC 3835
QY 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
Db 3836 CCCACAGCGCTGAACGCATCTCTTGACCCTCTCCAATTACATCTTACCCGAGTCTTTC 3895
QY 1333 euAlaGluMetThrValLysValValAlaLeuGlyTirPcysPheGlyGluGlnAlaTyrL 1353
Db 3896 TGGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTCTTCGGGAGCAGCGGTACC 3955
QY 1353 euArgSerSerTirPAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
Db 3956 TCGGAGCAGTTGGAACTGTGTGGACGGGCTGTTGGTGTCTCATCTCCGTTCATCGACATTC 4015
QY 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db 4016 TGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTGCGGC 4075
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db 4076 TGCTGCGGACCTTCCGCCCTCAGGGTGATCAGCGGCGCAGGGGCTGAAGCTGGTGG 4135
QY 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaP 1433
Db 4136 TGGAGACGCTGATGTCTCTCACTGAAACCCCATCGGCAACATTTGTAGTTCATCTGTGCT 4195
QY 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db 4196 TCITTCATCATTTTCGGCATCTTGGGGTGCAGCTCTCAAAGGGAAGTTTTTCGTGTGCC 4255
QY 1453 lnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473
Db 4256 AGGCGCAGGATACCAGGAACATCACCAATAAATCGGACTGTGCCAGGCCAGTACCGGT 4315
QY 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4316 GGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTCGTTT 4375
QY 1493 euAlaSerLysAspGlyTirPValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db 4376 TGGCCTCCAAGGATGGTTGGTGGACATCATGTACGATGGGCTGGATGCTGTGGCGTGG 4435
QY 1513 spGlnGlnProIleMetAsnHisAsnProTirPmetLeuLeuTyrPheIleSerPheLeuL 1533
Db 4436 ACCAGCAGCCCATCATGAACCAACACCCCTGGATGCTGTACTTTTCATCTCTGTTCTGCTGC 4495
QY 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4496 TCATTGTGGCCTTCTTTGTCTGAACATGTTTGTGGGTGTGGTGGAGAACTTCCACA 4555
QY 1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
Db 4556 AGTGTGGCAGCACCCAGGAGAAAGAGGAGGCCCGCGCGGAGGAGAGCGCCTACGAA 4615
QY 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProt 1593

||||| 4616 GACTGGAGAAAGAGAAGG-----AAAGCCAGTGCAAACCTT 4654
QY yrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL 1613
Db ACTACTCCGACTACTCCCGCTTCGGGCTCCGTCACCACTTGTGCACCCAGCCACTACC 4714
QY euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633
Db TGGACCTCTTCATACAGGTGTCTCGGGCTGAACGTGGTTCACCATGGCCATGGAGCACT 4774
QY yrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1653
Db ACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCA 4834
QY lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673
Db TCTTTGTCTTGGAGTCAGTTTCAAACCTTGTGGCCCTTTGGTTTCCGTCCGTCTTCCAGG 4894
QY spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693
Db ACAGGTGGAACCACTGGACCTGGCCATTGTGCTGTCCATCATCGGCATCACGCTGG 4954
QY luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713
Db AGGAAATCGAGGTCAACGCCTCGCTGCCCATCAACCCCAACCATCATCCGCATCATGAGG 5014
QY alIleuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuL 1733
Db TGTGCGCATTTGCCCGAGTGTGAAGCTGCTGAAGATGGCTGTGGGCATCGGGCGCTGC 5074
QY euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
Db TGGACACGGTGTATGCAGGCTGCCCCAGGTGGGGAACCTGGGACTTCTTTCATGTTGT 5134
QY euPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773
Db TGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGA 5194
QY hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
Db CACACCCCTGTGAGGGCCTGGGCGGTATGCCACCTTTTCGGAACCTTTGGCATGGCCTTCC 5254
QY euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813
Db TAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTTATGAAGACACCCCTCC 5314
QY rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS 1833
Db GGGACTGTGACCAGGAGTCCACCTGTCTACAACACGGTCACTCGCCTATCTACTTTGTGT 5374
QY erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853
Db CCTTCGTGTGACGGCCCCAGTTCTGTAGTCAACGTGGTGTATCGCCGTGCTGATGAAGC 5434
QY isLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuL 1873
Db ACCTGGAGGAGAGCAACAAGAGGCGCAAGGAGCGAGCTAGAGGTGAGCTGGAGC 5494
QY euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP 1893
Db TGGAGATGAAGACCCCTCAGCCCCCAGCCCCCACTCGCCACTGGGCCTTCCTCTGGC 5554
QY roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
Db CTGGGTGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCCAGCGG 5614
QY laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933
Db CCCACGCGAGATCAGCCTCCCACTTTTCCCTGGAGCACCCCAACGATGCAGCCCCACCCCA 5674
QY luGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerA 1953
|||||

Db 5675 CGGAGCTGCCA-----GGACCAGACTTACTGACTGTGCGGAAGTCTGGGTCAGCC 5725
QY rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgs 1973
Db GAACGCACTCTTGCCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGC 5785
QY erLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993
Db CCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAAGGCTCCGTCTTGTCCGTTC 5845
QY isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL 2013
Db ACTCCCAGCCAGCAGATACCAAGTACATCTCTGCAGCTTCCCAAAGATGCACCTCATCTGC 5905
QY euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgs 2033
Db TCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACCAAGGAGCT 5965
QY erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053
Db CCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAATAAGGACTGACTCTCTTGGAGC 6025
QY alGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073
Db TTCAGGCTCTGGCAGCCGGGAAGACTGTGGCAGAGGTGAGTGGGCCCTCCCCGCCCC 6085
QY euThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnArgSerGlyI 2093
Db TGGCCCGGGCCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCA 6145
QY leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
Db GCCACAGCAAGATCTCCAAGCACATGACCCCCGCCAGCCCTTGCACAGGCCCAACCCA 6205
QY erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
Db ACTGGGGCAAGGGCCCTCCAGAGACCAGAAAGCAGCTTAGAGTTGGACACGGAGCTGAGCT 6265
QY rpIleSerGlyAspLeuLeu---ProSerSerGlnGluGluProLeuPheProArgAspL 2152
Db GGATTTTCAGGAGACCTCTCTGCCCCCTGGCGGCCAGGAGGAGGCCCCCATCCCCACGGGACC 6325
QY euLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuA 2172
Db TGAAGAAGTGTACAGCGTGGAGGCCACAGAGCTGCCAGCGCGGCTACGTCTCGTGGCTGG 6385
QY spGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgL 2192
Db ATGACGACAGGAGACACTCTATCGCCGTGAGTGCCTGGACAGCGGCTCCCAACCCCAACC 6445
QY euCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProL 2212
Db TGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGGCTGGGAGCCGGCCCA 6505
QY ysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgP 2232
Db AGAAAAAACTCAGCCCGCCTAGTATCACCATAGACCCCCCGAGAGCCCAAGGTCTCTCGGA 6565
QY roProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAspSerLysAspP 2252
Db CCCCGCCCTCTGGCCCCCTGACAGCATGGTGTCTCGCCCTCCCAAAAGAAAGATGTGC 6625
QY roSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrL 2272
Db CCTTGGCCTCTGGCCCCCTGACAGCATGGTGTCTCGCCCTCCCAAAAGAAAGATGTGC 6685
QY euSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db TGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGGACCC 6729

RESULT 13
AAF31684
ID AAF31684 standard; cDNA; 6892 BP.

XX AAF31684;
AC
XX
DT 09-APR-2001 (first entry)
XX Human alpha-IG T-type calcium channel cDNA.
DE
XX
KW Human; antiarrhythmic; anticonvulsant; hypotensive; cardiac; nootropic;
KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel;
KW ss.
XX
OS Homo sapiens.
XX WO200102561-A2.
PN
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-CA000794.
XX
PR 02-JUL-1999; 99US-00346794.
XX
PA (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI Snutch TP, Baillie DL;
XX
DR WPI; 2001-123111/13.
DR P-PSDB; AAB66481.
XX
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
PS Example 3; Fig 6; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX
SQ Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6892
Score: 10916.00 Matches: 2109
Percent Similarity: 93.42% Conservative: 34
Best Local Similarity: 91.94% Mismatches: 113
Query Match: 90.75% Indels: 38
DB: 5 Gaps: 6

US-09-611-257A-24 (1-2287) x AAF31684 (1-6892)

QY 19 AlaArgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArg 38
DB 7 GCTTGCCCTCTCCGGATCGCCCGGGGCCCGGCTGGCCAGAGGATGGACGAGGAGG 66

QY 39 MetGluArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCys 58
DB 67 ATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGGAGCTTCATCGGGCTCAACGACCTGT 126

QY 59 ProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAsps 78
DB 127 CGGGGGCCGGGGCCGGCCGGGGCGGGGTGACGAGAAAAGGACCCGGGCGCGGACT 186

QY 78 erGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerG 98
DB 187 CCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTTTCTTCTACTTGAGCC 246

QY 98 InAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgV 118
DB 247 AGGACAGCCGCCCGGAGCTGGTGTTCTCCGCACGGTCTGTAAACCCCTGGTTTGAGCGCA 306

QY 118 alSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluA 138
DB 307 TCAGCATGTTGGTCATCCTTCTCAACTGCGTGACCTGGGCATGTTCCGGCCATGCGAGG 366

QY 138 spIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheA 158
DB 367 ACATCGCCTGTGACTCCCGAGCGCTGCCGATCCTCAGGCCTTTGATGACTTCATCTTTG 426

QY 158 laPhePheAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysLysC 178
DB 427 CCTTCTTTGCCGTGGAGATGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAAAAGT 486

QY 178 ysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuG 198
DB 487 GTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGATGCTGG 546

QY 198 luTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuA 218
DB 547 AGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGTGTTCAGACAGTCCGCTGTGCTGC 606

QY 218 rgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuA 238
DB 607 GACCGCTCAGGGCCATTAAACCGGTGCCAGCATGCGCATCCTTGTACAGTTGCTGCTGG 666

QY 238 spThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheG 258
DB 667 ATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTG 726

QY 258 lyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluA 278
DB 727 GCATCGTCGGCGTCCAGCTGTGGGCAGGGCTGCTTCGGAACCGATGCTTCTTCTTCTGAGA 786

QY 278 snPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspG 298
DB 787 ATTTCAGCCTCCCCCTGAGCGTGACCTGGAGCGCTATTACCAGACAGAGAAGAGGATG 846

QY 298 luSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValP 318
DB 847 AGAGCCCTTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGGTCTTGCAGAAAGCGTGC 906

QY 318 roThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrA 338
DB 907 CCACGCTGCGGGGACGCGGGCGGTGGCCCCACCTTGGCGTCTGGACTATGAGGCCTACA 966

QY 338 snSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaG 358
DB 967 ACAGCTCCAGCAACACCACTGTGTCAACTGGAACTACTACACCAACTGCTCAGCGG 1026

QY 358 lyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378
DB 1027 GGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACATTGGCTATGCTGGATCG 1086

QY 378 laIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspA 398
DB 1087 CCATCTTCCAGGTCAACGCTGGAGGGCTGGGTCCGACATCATGTACTTTTGTGATGGATG 1146

QY 398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheM 418
DB 1147 CTCATTCTTCTACAATTTTCATCTACTTTCATCCTCTCTCATCATCGTGGGCTCTTCTTCA 1206

QY 418 etIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
DB 1207 TGATCAACCTGTGCTGCTGGTGAATGGCCAGCAGTTCTCAGAGACCAAGCAGCGGGAAA 1266

QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
DB 1267 GCCAGCTGATCGGGAGCAGCGTGTGCGGTTTCCCTGTCCAACGCCAGCACCTGGCTAGCT 1326

QY 458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478

Db 1327 TCTCTAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTAGCTACCTGGTGATACATCCTTCGTA 1386
Qy 478 ysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeus 498
Db 1387 AGGAGCCCGCAGGCTGGCTCAGGTTCTCTCGGCAGCAGGTTGTGGGCTTGGCGTCTCA 1446
Qy 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
Db 1447 GCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCTGCTCTCGCTCCC 1506
Qy 518 isArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHis 538
Db 1507 ACCCGCGCTATCCGTCACACCTGGTGACACCAACCACCACTACCACTACC 1566
Qy 538 isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
Db 1567 ACCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGGATG 1626
Qy 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
Db 1627 CCAATGGTCCCGCAGGCTCATGCTGCCACCACTCGACGCCTGCCCTCTCCGGGGCCC 1686
Qy 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
Db 1687 CCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCAGTCCGACTTAGAGCCAG 1746
Qy 598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlys 618
Db 1747 TCCGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCCGGCAGGACTGTGGGCA 1806
Qy 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
Db 1807 GCGGGAAGGTGTATCCCAACCGTGCACACCAGCCCTCCACGGAGACGCTGAAGGAGAAG 1866
Qy 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProp 658
Db 1867 CACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACAGCCTCAACATCCCAC 1926
Qy 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
Db 1927 CCGGGCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGTACAGGTGCCTGCCAAA 1986
Qy 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAsps 698
Db 1987 GCTCTTGAAGATCTCCAGCCCTGCTTGAAGCAGACAGTGGAGCCTGTGGTCCAGACA 2046
Qy 698 erCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetP 718
Db 2047 GCTGCCCTACTGTGCCCGGGCGGGGAGGTGGAGCTCGCCGACCGTGAATGC 2106
Qy 718 roAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuA 738
Db 2107 CTGACTCAGACAGCGAGCGAGTTATGAGTTTACACAGGATGCCAGCACAGCAGCTCC 2166
Qy 738 rgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerV 758
Db 2167 GGGACCCCCACAGC---CGGGCGCAACGGAGCCTGGGCCCAGATGCAGAGCCAGCTCTG 2223
Qy 758 alLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrP 778
Db 2224 TGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTGGACAGCAAGTACT 2283
Qy 778 heGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrH 798
Db 2284 TTGGCCGGGAATCATGATCGCCATCCTTGGTCAACACTCAGCATGGGCATCGAATACC 2343
Qy 798 isGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerL 818
Db 2344 ACGAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTCACCAGCC 2403
Qy 818 euPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysA 838

Db 2404 TCTTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTTGGCTACATCAAGA 2463
Qy 838 snProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyG 858
Db 2464 ATCCCTACAAACATCTTCGATGGTGTTCATTTGGTTCATCAGCGTGTGGAGATCGTGGCC 2523
Qy 858 lnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuV 878
Db 2524 AGCAGGGGGGGCCCTGTCGGTGTTCGGACCTTCCGCCGTGATGCGTGTGCTGAAGCTGG 2583
Qy 878 alArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnV 898
Db 2584 TCGCTTCCCTCGCGGCTGCAGCGGCAGCTGGTGTGCTCATGAAGACCATGGACAACG 2643
Qy 898 alAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMeth 918
Db 2644 TGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTTCATCTTCAGCATCCTGGGCATGC 2703
Qy 918 isLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysA 938
Db 2704 ATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCCCTGCCAGACCGGAAGA 2763
Qy 938 snPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspT 958
Db 2764 ATTTTGACTCCTTGTCTCTGGCCATCGTCACTGTCTTTCAGATCTTGACCCAGGAGACT 2823
Qy 958 rpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheI 978
Db 2824 GGAACAAAGTCCTCTACAATGGTATGSCCTCCACGTCGTCCTGGCGGCCCTTTATTTCA 2883
Qy 978 leAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValG 998
Db 2884 TTGCCCTCATGACTTCGGCAACTACGTGCTCTTCAATTTGCTGTGCGCATTTCTGTGTG 2943
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Qy 1004 -----GlyAspAlaThrLysSerGluSerGluProAspP 1015
Db 3004 TTCAGTGCCTGTGACTCCAGGGGGAGATGCCAACCAAGTCCGAATCAGAGCCCGATT 3063
Qy 1015 hePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaL 1035
Db 3064 TCTTCTCACCCAGCTGGATGGTGTATGGGACAGGAAGATGCTTGGCCTTGGTGTCCC 3123
Qy 1035 euGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaA 1055
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Qy 1055 laThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerG 1075
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Qy 1075 lySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetL 1095
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Db 3421 CAAGTGGAGAGCGCGGCTGCTTGTTCGGGAGAAGGCCAGGAGCCAGGATGAAGAGG 3480
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Qy 1235 spAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgL 1255
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Qy 1255 euProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerA 1275
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Db CCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTGCGGCTGCTGC 4200
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Qy 1415 hrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheI 1435
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Qy 1475 rgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlas 1495
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QY 2234 ysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerV 2254
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RESULT 14
ADQ89063
ID ADQ89063 standard; cDNA; 7648 BP.
XX
AC ADQ89063;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human urological disorder related protein 4421 encoding cDNA SEQ.15.
XX
KW urological disorder; uropathic; cytostatic; urinary incontinence;
KW benign prostatic hyperplasia; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..7134
FT /*tag= a
FT /product= "urological disorder related protein 4421"
XX
PN WO2004065576-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004WO-US0000750.
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0499594P.
PR 26-SEP-2003; 2003US-0506332P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Karicheti V, Silos-Santiago I, Eliasof SD;
XX
DR WPI; 2004-562167/54.
XX P-PSDB; ADQ89064.
PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
PT disorder.
XX
PS Claim 1; SEQ ID NO 15; 542pp; English.
XX
CC The present invention describes the use of polypeptides related to
CC urological disorders for identifying a compound capable of treating a
CC urological disorder, identifying a subject having a urological disorder,
CC or treating a subject having a urological disorder. Also described: (1) a
CC method for identifying a compound capable of treating a urological
CC disorder; (2) a method for identifying a subject having a urological
CC disorder; and (3) a method for treating a subject having a urological
CC disorder. The compound has uropathic and cytostatic activities. The
CC polypeptides related to urological disorders are useful for identifying a
CC compound capable of treating a urological disorder, identifying a subject
CC having a urological disorder, or treating a subject having a urological
CC disorder. Disorders include urinary incontinence and benign prostatic
CC hyperplasia. The present sequence encodes a human urological disorder
CC related protein, which is used in the exemplification of the present
CC invention.
XX

SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	7648
Score:	10845.50	Matches:	210
Percent Similarity:	89.72%	Conservative:	33
Best Local Similarity:	88.33%	Mismatches:	110
Query Match:	90.17%	Indels:	135
DB:	13	Gaps:	7

US-09-611-257A-24 (1-2287) x ADQ89063 (1-7648)

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QY	54	SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspp	73
DB	62	GGCTCAACGACCTGTTCGGGGCCGGGGCCGGCCGGGGTTCAGCAGAAAAGGACC	121
QY	73	roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP	93
DB	122	CGGGCAGCGCGACTCCGAGGGCGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTTT	181
QY	93	hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP	113
DB	182	TCTTCTACTTGAGCCAGGACAGCCGCCGCGGAGCTGGTGCTCCGCACGGTCTGTAAAC	241
QY	113	roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP	133
DB	242	CCTGGTTTGAGCGCATCAGCATGTTGGTCATCCTTCTCACTGCGTGACCCCTGGGCATGT	301
QY	133	heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA	153
DB	302	TCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTG	361
QY	153	spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI	173
DB	362	ATGACTTTCATCTTTGGCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCITGGGCA	421
QY	173	lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI	193
DB	422	TCTTTGGGAAAAGTGTTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA	481
QY	193	leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
DB	482	TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTACAGTTCTCAGCTGTGAGGA	541
QY	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
DB	542	CAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTTG	601
QY	233	alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV	253
DB	602	TCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCTGTGTCTCTGCTTCG	661
QY	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
DB	662	TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAAACCGAT	721
QY	273	ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
DB	722	GCTTCCCTACCTGAGAAATTTCAGCCTCCCTTGAGCGTGGACCTGGAGCGCTATTACCGA	781
QY	293	hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
DB	782	CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACCGCATGCGGT	841
QY	313	erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA	333
DB	842	CCTGCAGAAAGCTGCCACGCTGCGCGGGGACGCGGGCGGTGGCCACCTTGGCGGTCTGG	901
QY	333	spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353

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Db 2399 TTGGCTTACATCAAGAAATCCCTACAAACATCTTCGATGGTGTCTATTGTGTCATCAGCGTGT 2458

Qy 853 rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873

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Qy 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA 1110

Db 3239 CC--CACGAGATGAAGTACCGCCCGCAGCGCCCGCAGCTCTCCGACAGCCCTGGAGCG 3295

Qy 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130

Db 3296 CTGCAAGCAGCTGGACACAGCAGCGCTCCAGCCCGAAACAGCCTCGGCCGTGCACCCAGCC 3355

Qy 1130 euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluS 1150

Db 3356 TGAAGCGGAGAACCCAAAGTGGAGAGCGCGGTCCCTGTGTGCGGAGAAGGCCAGGAGA 3415

Qy 1150 erGlnAspGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170

Db 3416 GCCAGGATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCCGCCCTCGGGCAGTGACCATC 3475

Qy 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190

Db 3476 GCCACAGGGGTCCCTGGAGCGGGAGGCCAAAGATTCCTTTGACCTGCCAGACACACTGC 3535

Qy 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210

Db 3536 AGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAAGACT 3595

Qy 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230

Db 3596 GCAATGGCAAGTCGGCTTCAGGGCGCTGCGCCCGGCCCTCGGGCCTGATGACCCCCCAC 3655

Qy 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250

Db 3656 TGGATGGGATGACCGCGATGACGAGGGCAACCTGAGCAAGGGGAAACGGTCCGCGCGT 3715

Qy 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270

Db 3716 GGATCCGAGCCCCGACTCCCTGCCTGCTGCTCGAGCGAGACTCCTGGTCAGCCTACATCT 3775

Qy 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290

Db 3776 TCCCTCCTCAGTCCAGGTTCCGCCCTCCTGTGTACCCGGATCATCACCAAGATGTTTCG 3835

Qy 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310

Db 3836 ACCACGTGGTCTTGTTCATCATCTTCTCTTAATGTCATCACCATCGCCATGGAGCGCCCA 3895

Qy 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330

Db 3896 AAATTGACCCCCACAGCGCTGAACGCATCTTCTCTGACCCCTCTCCAATTACATCTTCACCG 3955

Qy 1330 laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluG 1350

Db 3956 CAGTCTTCTGGCTGAAATGACAGTGAAGGTGGTGGCAGTGGGCTGGTCTTCGGGGAGC 4015

Qy 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerValI 1370

Db 4016 AGGCGTACCTGCGGAGCAGTGGAAACGTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTCA 4075

Qy 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390

Db 4076 TCGACATTTCTGGTGTCCATGCTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGG 4135

Qy 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410

Db 4136 TGCTGGGCTGTCTGCGGACCCCTGCCCCGCTCAGGGTGATCAGCCCGGCGCAGGGGCTGA 4195

QY 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
DB 4196 AGTGGTGGAGACGCTGATGTCCTCACTGAAACCCATCGGCAACATTGTAGTCATCT 4255
QY 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
DB 4256 GCTGTGCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTT 4315
QY 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
DB 4316 TCGTGTGCCAGGCGAGGATACCAAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCA 4375
QY 1470 erTyrArgTrpValArgHisLysTyrAsnPheAspAsnIleuGlyGlnAlaLeuMetSerL 1490
DB 4376 GTTACCGGTGGGTCGGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCC 4435
QY 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlav 1510
DB 4436 TGTTCGTTTGGCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTG 4495
QY 1510 alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIles 1530
DB 4496 TGGGCGTGGACCAGCAGCCCCATCATGAACCAACACCCCTGGATGCTGCTACTTCATCT 4555
QY 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
DB 4556 CGTTCCCTGCTCATTTGTGGCTTCTTTGTCCTGAACATGTTTGTGGGTGTGGTGGAGA 4615
QY 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysA 1570
DB 4616 ACTTCCACAAGTGTGGCAGCACCCAGGAGGAAGAGGAGGCCCGCGCGGGAGGAGAAGC 4675
QY 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
DB 4676 GCCTACGAAGACTGGAGAAAAGAGAAGGAATCTAATGCTGGACGATGTAATTGCTTCCG 4735
QY 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
DB 4736 GCAGCTCAGCCAGCGCTGCGTCAGAAGCCCACTGCAAAACCTTACTACTCCGACTACTCCC 4795
QY 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG 1619
DB 4796 GCTTCGGGCTCCTCGTCCACCACTTGTGCACCAGCCACTACCTGGACCTTTCATCACAG 4855
QY 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
DB 4856 GTGTCTCGGGCTGAACGTGGTCACCATGGCCATGGAGCACTACCAGCAGCCCAAGATT 4915
QY 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
DB 4916 TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTTCATCTTTGTCTTGGAGTCAG 4975
QY 1659 alPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuA 1679
DB 4976 TTTTCAAACCTGTGGCCTTTTGGTTTCCGTCGGTTCTTCCAGGACAGGTGGAACCAAGCTGG 5035
QY 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
DB 5036 ACCTGGCCATTGTGCTGCTGCCATCATGGCATCATCGGATCATGAGGGTGTGCGCATTGGCCGAG 5095
QY 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
DB 5096 CCTCGCTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGTGCGCATTGGCCGAG 5155
QY 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
DB 5156 TGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACCGGTGATGCAGG 5215
QY 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
DB 5216 CCCTGCCCAAGGTGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGTCAG 5275
QY 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779

DB 5276 CTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTCTGTAGGGCC 5335
QY 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
DB 5336 TGGGCGTTCATGCCACCTTTCGGAACCTTTGGCATGGCCTTCTTAACCTCTTCCGAGTCT 5395
QY 1799 erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
DB 5396 CCACAGGTGACAAATTGGAATGGCATATTGAAGGACACCCCTCCGGACTGTGACACAGGAGT 5455
QY 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
DB 5456 CCACCTGTACAACACGGTCACTCGCCTATCTACTTTGTGTCTCTTCGTGCTGACGGCCC 5515
QY 1839 lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
DB 5516 AGTTCGTGCTAGTCAACGTGGTGATCGCCGTGCTGATGAAGCACCTGGAGGAGAGCAACA 5575
QY 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuS 1879
DB 5576 AGGAGCCCAAGGAGGAGGCGGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCA 5635
QY 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
DB 5636 GCCCCAGCCCCACTCGCCACTGGGACGCCCTTCTCTGGCCTGGGGTTCAGGGGCCCCG 5695
QY 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
DB 5696 ACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCCT 5755
QY 1919 erGlyPheSerLeuGluHisProThr----- 1927
DB 5756 CCCACTTTTCCCTGGAGCACCCCAACCGACGACAGGAGCTGTTTGACACCATATATCCCTGTGA 5815
QY 1927 ----- 1927
DB 5816 TCCAGGGCTCCCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCCAGGGGGCC 5875
QY 1927 ----- 1927
DB 5876 AGCCCTCTGCCTTCCCTTCTGCCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAG 5935
QY 1927 ----- 1927
DB 5936 CTGAGATGGAGGCTCTGTCTCTGACGTCAGAGATTGTGTCTGAACCCGTCCTGCTCTCTAG 5995
QY 1927 ----- 1927
DB 5996 CTCTGACGGATGACTCTTTTGCCTGATGACATGACACACACTCTTACTTAGTGCCCTGGAGA 6055
QY 1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV 1946
DB 6056 GCAATATGCAGCCCCCAACCCACGAGCTGCCA-----GGACCAGACTTACTGACTG 6106
QY 1946 alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
DB 6107 TCGGGAAGTCTGGGGTCAGCCGAACGCACTCTCTGCCCAATGACAGCTACATGTGTCTGGC 6166
QY 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnS 1986
DB 6167 ATGGAGCACTGCCGAGGGGGCCCCCTGGGACACAGGGGCTGGGGCTCCCCAAAGCTCAGT 6226
QY 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
DB 6227 CAGGCTCCGTCTGTCCGTCACTCCAGCCAGCAGATACAGCTACATCTCCTGCAGCTTC 6286
QY 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL 2026
DB 6287 CCAAAGATGCACCTCATCTGCTCCAGCCCCACAGCCCCCAACCTGGGGCACCATCCCCA 6346
QY 2026 ysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046

Db 6347 AACTGCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAA 6406

Qy 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluV 2066

Db 6407 TAAGGACTGACTCCTTGGACGTTTCAAGGCTGGGACGCGGGAAGACCTGCTGGCAGAGG 6466

Qy 2066 alSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIleG 2086

Db 6467 TGAGTGGGCCCTCCCGGCCCTGGCCCGGCTACTCTTTTCTGGGCCAGTCAAGTACC 6526

Qy 2086 lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlap 2106

Db 6527 AGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCC 6586

Qy 2106 roCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuG 2126

Db 6587 CTTGCCAGGCCCCAGAACCCAACTGGGGCAAGGCCCTCCAGAGACCAGAGCAGCTTAG 6646

Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu--ProSerSerGlnGluG 2145

Db 6647 AGTTGGACACGGAGCTGAGCTGGATTTTCAGGAGACCTCTGCCCCCTGGCGGCCAGGAGG 6706

Qy 2145 luProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCysArgA 2165

Db 6707 AGCCCCATCCCCACGGGACCTGAAGAAGTGTACAGCTGGAGGCCAGAGCTGCCAGC 6766

Qy 2165 rgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCysLeuA 2185

Db 6767 GCCGGCTACGTCCTGGCTGGATGAGCAGAGGAGACACTCTATCGCCGTCAGTGCCTGG 6826

Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205

Db 6827 ACAGCGGCTCCCAACCCCACTGGGCACAGACCCCTCTAACCTTGGGGCCAGCCTCTTG 6886

Qy 2205 lyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProp 2225

Db 6887 GGGGGCTGGGAGCGCGCCCAAGAAAAAACTCAGCCGCTAGTATCACCATAGACCCCC 6946

Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlap 2245

Db 6947 CCGAGACCAAGTCTCTCGGACCCCGCCAGCCCTGGTATCTGCTCCGAGGAGGCTC 7006

Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265

Db 7007 CGTCCAGGACTCCAAGGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCCTGC 7066

Qy 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMeta 2285

Db 7067 CCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCCTCTGACCCAGCAGACCTGG 7126

Qy 2285 spPro 2286

Db 7127 ACCCC 7131

RESULT 15

ADS16298

ID ADS16298 standard; DNA; 7648 BP.

XX

AC ADS16298;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human voltage-dependent alpha 1G subunit calcium channel (CACNA1G) DNA.

XX

KW Voltage-dependent ion channel; drug candidate;

KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;

KW anticonvulsant; antiarrhythmic; human; alpha 1G subunit; ds.

XX

OS Homo sapiens.

XX

PN US2004175761-A1.

XX

PD 09-SEP-2004.

XX 01-MAR-2003; 2003US-00377139.

PF

XX 01-MAR-2003; 2003US-00377139.

PR

XX (MACK/) MACKINNON R.

PA (MACK/) MACKINNON A L.

PA (JIAN/) JIANG Y.

PA (RUTA/) RUTA V.

XX

PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;

XX WPI; 2004-642122/62.

DR REFSEQ; NM_018896.

XX

PT Screening drug candidates that target voltage dependent ion channel

PT protein, involves contacting screening protein with chemical compound,

PT which is drug candidate and determining whether chemical compound binds

PT to screening protein.

XX

PS Disclosure; SEQ ID NO 10; 6lpp; English.

XX

CC The invention relates to the composition of matter suitable for use in

CC identifying chemical compounds that bind to voltage-dependent ion channel

CC proteins. The composition comprises a screening protein that consists of

CC an ion channel voltage sensor domain of the ion channel protein

CC immobilised on a solid support. The invention is useful for identifying

CC chemical compounds (drug candidate) that bind to voltage-dependent ion

CC channel proteins. The drug candidate of the invention is utilised for

CC treating a condition mediated by aberrant electrical activity that

CC initiates uptake or release of neurotransmitters and contraction of

CC muscles. The drug candidate of the invention is also utilised for

CC treating epilepsy and arrhythmia. The present sequence is a voltage-

CC dependent calcium channel DNA.

XX

SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7648

Score: 10845.50 Matches: 2105

Percent Similarity: 89.72% Conservative: 33

Best Local Similarity: 88.33% Mismatches: 110

Query Match: 90.17% Indels: 135

DB: 13 Gaps: 7

US-09-611-257A-24 (1-2287) x ADS16298 (1-7648)

Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53

Db 2 TGGACGAGGAGGAGATGGAGCGGGCGCGGAGGAGTCGGGACAGCCCGGAGCTTCATGC 61

Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73

Db 62 GGCTCAACGACCTGTGGGGCGCGGGGCGCGGGCGCGGGGTCAGCAGAAAGGACC 121

Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93

Db 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGTGCGGTACCCCGCGCTGGCCCGGTGTTT 181

Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCTTCTACTTGAGCCAGGACAGCCCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAAAC 241

Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CTGGTTTGAGCGCATCAGCATGTTGGTTCATCCTTCTCAACTGCGTGACCCCTGGGCATGT 301

Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153

Db 302 TCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCTTTG 361

Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTGGCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGCA 421

QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193

Db 422 TCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACGGCTTGACTTTTTCATCGTCA 481

QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213

Db 482 TCGCAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCA 541

QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGCCATTAAACCGGTGCCAGCATGCGCATCTTG 601

QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253

Db 602 TCACGTTGCTGTGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTCTCTTCG 661

QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273

Db 662 TCTTCTTCATCTTCGGCATCGTCGGCTCCAGCTGTGGCAGGGCTGCTTCGGAAACCGAT 721

QY 273 yspHeLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293

Db 722 GCTTCTCTACCTGAGAAATTCAGCCTCCCTTGAGCGTGGACCTGGAGCGCTATTAC 781

QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313

Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCACGCGAGAACGGCATGCGGT 841

QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyG 333

Db 842 CCTGCAGAACGCTGCCACGCTGCGGGGGACGGGGGGCGGTGGCCCCACCTTGC 901

QY 333 spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353

Db 902 ACTATGAGCGCTACAACAGCTCCAGAACACACACCTGTGTCAACTGGAAACAGTACTACA 961

QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValaIleAsnPheAspAsnIleG 373

Db 962 CCAACTGCTCAGCGGGGGAGACAAACCCCTTCAAGGGCGCATCAACTTTGACAAACATTG 1021

QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393

Db 1022 GCTATGCTGTGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGCTGGTTCGACATCATGT 1081

QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413

Db 1082 ACTTTGTGATGGATGCTCATTTCTTCTACAAATTTTCATCTACTTTCATCTCTCATCATCG 1141

QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433

Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGTGATGCCACGCAGTTCTCAGAGA 1201

QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453

Db 1202 CCAAGCAGCGGAAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCTCTGTCCAACGCCA 1261

QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473

Db 1262 GCACCCCTGGTAGCTTCTCTGAGCCCGGCAGCTGCTATGAGGAGCTGTCTCAAGTACCTGG 1321

QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVala 493

Db 1322 TGTACATCTCTCGTAAGGACGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381

QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513

Db 1382 GGGTTGGGCTGCTCAGCAGCCCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441

QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533

Db 1442 GCTGCTCTCGTCCACCCGCCCTATCCGTCCACCACTGGTGCACCAACCACCAACCACC 1501

QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553

Db 1502 ATCACCAACACTACCACTGGCAATGGACGCTCAGGCCCCCGGGCCAGCCCGGAGA 1561

QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573

Db 1562 TCCAGGACAGGGATGCCAATGGTCCCGCAGGCTCATGTGCCACCACTCGAGCCTG 1621

QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CCCTCTCCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681

QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613

Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCCG 1741

QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633

Db 1742 GCAGGACTGTGGCAGCGGGAAGGTGTATCCCACTGCACACAGCCCTCCACCGGAGA 1801

QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653

Db 1802 CGTGAAGGAGAAGGCACTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861

QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673

Db 1862 GCCTAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGTA 1921

QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693

Db 1922 CAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGATGGAG 1981

QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713

Db 1982 CCTGTGTTCCAGACAGCTGCCCTACTGTGCCCGGGCGGGCAGGGAGGTGGAGCTCG 2041

QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733

Db 2042 CCGACCGTGAAATGCCTGACTCAGACAGCGAGGAGTTATGAGTTTCAACACAGGATGCC 2101

QY 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753

Db 2102 AGCACAGCGACCTCCGGGACCCCAACAGC --- CGCGCGCAACGGAGCCTGGGCCAGATG 2158

QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773

Db 2159 CAGAGCCAGCTCTGTGTGCGCTTCTTGAGGCTAATCTGTGACACCTTCGAAAAGATTG 2218

QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793

Db 2219 TGGACAGCAAGTACTTTGGCGGGGAATCATGATCGCATCTCTGGTCAACACACTCAGCA 2278

QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813

Db 2279 TGGGATCGAATACCAACGAGAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338

QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProp 833

Db 2339 TCGTCTTCAACAGCCTCTTTGCCCTTGAGATGCTGTGTAAGCTGTGTGTATGGTCCCT 2398

QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853

Db 2399 TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGTGTTCATTTGTGTCATCAGCGTGT 2458

QY 853 rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873

Db 2459 GGGAGATCGTGGGCCAGCAGGGGGGGCGGCTGTTCGGTGTCTCGGACCTTCCGCTGATGC 2518

QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893

Db 2519 GTGTGCTGAAGCTGGTGCCTTCTTCCGGCGCTGCAGCGGAGCTGGTGGTGTCTCATGA 2578

QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhePheS 913
Db 2579 AGACCATGGACAACGTGGCCACCTTCTGCATGCTGTATGCTCTCATCTTCATCTTCA 2638
QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
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QY 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TCGCCATTCTGGTGGAGGCTTCCAGCGGAGGAATCAGCAAAACGGGAAGATGCGAGTG 2938
QY 1004 -----GlyAspAlaThrLysSerG 1010
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QY 1010 luSerGluProAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgL 1030
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Db 3059 TGGCCTTGGTGTCCCTGGGAGAGCACCCGGAGTGGGAAGAGCCTGCTGCCCTCTCA 3118
QY 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
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QY 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250

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Qy 1927 ----- 1927

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Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
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Qy	2265	roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMeta	2285
Db	7067	CCTCCCCAAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCCTCTGACCCAGCAGACCTGG	7126
Qy	2285	spPro	2286
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Search completed: April 28, 2005, 09:29:50
Job time : 2269 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 28, 2005, 07:51:47 ; Search time 527 Seconds
(without alignments)
7100.882 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
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Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -ENDs=1 -MATRIX=biosum62 -TRANS=human40.cdi
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Database : Issued_Patents_NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11066.5	92.0	7741	3	US-09-426-998-4
2	10948.5	91.0	6822	3	US-09-426-998-3
3	10739	89.3	7405	4	US-09-949-016-3859
4	6241	51.9	7898	3	US-08-984-709A-49
5	6103	50.7	3993	4	US-09-398-522-51
6	5420	45.1	6816	3	US-09-404-650-1
7	5420	45.1	6816	4	US-09-935-541-1
8	5420	45.1	6855	3	US-09-404-650-3
9	5420	45.1	6855	4	US-09-935-541-3
10	5407	45.0	6503	3	US-09-404-650-12
11	5407	45.0	6503	4	US-09-935-541-12
12	2055	17.1	70308	4	US-09-949-016-15601

13	1974	16.4	1669	3	US-08-984-709A-51	Sequence 51, Appli
14	1745.5	14.5	7362	1	US-08-455-543A-7	Sequence 7, Appli
15	1745.5	14.5	7362	2	US-08-193-078B-7	Sequence 7, Appli
16	1745.5	14.5	7362	2	US-08-223-305C-7	Sequence 7, Appli
17	1745.5	14.5	7362	2	US-08-149-097D-7	Sequence 7, Appli
18	1745.5	14.5	7362	3	US-08-949-386-7	Sequence 7, Appli
19	1745.5	14.5	7362	3	US-08-450-562-7	Sequence 7, Appli
20	1745.5	14.5	7362	3	US-08-984-709A-7	Sequence 7, Appli
21	1745.5	14.5	7362	3	US-08-450-272-7	Sequence 7, Appli
22	1745.5	14.5	7362	4	US-08-450-273-7	Sequence 7, Appli
23	1743.5	14.5	7376	3	US-09-268-163-3	Sequence 3, Appli
24	1740.5	14.5	7266	3	US-08-713-118-1	Sequence 1, Appli
25	1740.5	14.5	7266	3	US-09-452-007-1	Sequence 1, Appli
26	1739.5	14.5	7364	3	US-09-268-163-5	Sequence 5, Appli
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42	1693	14.1	7011	3	US-09-268-163-9	Sequence 9, Appli
43	1691	14.1	5975	1	US-08-336-257A-3	Sequence 3, Appli
44	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025
45	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025

ALIGNMENTS

RESULT 1
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11066.50 Matches: 2134
Percent Similarity: 93.81% Conservative: 33
Best Local Similarity: 92.38% Mismatches: 112
Query Match: 92.01% Indels: 31
DB: 3 Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-426-998-4 (1-7741)

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QY	43	ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly	62
Db	551	CCGAGGAGTCGGGACAGCCCGGAGCTTCATCGGGCTCAACGACCTGTCCGGGGCCGGG	610
QY	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG	82
Db	611	GCCGGCCGGGCGGGGTCCAGCAGAAAAGACCCGGGCAGCGCGACTCCGAGGCGGAGG	670
QY	82	lyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP	102
Db	671	GGCTGCCGTACCCGGCGTGGCCCGGCTGTGTAAACCCCTGGTTTGAGCGCATCAGCATGTTGG	730
QY	102	roArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuV	122
Db	731	CGCGAGCTGGTGTCTCCGCACGGTCTGTAAACCCCTGGTTTGAGCGCATCAGCATGTTGG	790
QY	122	allLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142
Db	791	TCATCCTTCTCAACTGCTGACCTGGGCATGTTCCGGCCATGCGAGGACATCGCCTGTG	850
QY	142	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaV	162
Db	851	ACTCCAGCGCTGCCGGATCCTGCAGGCCCTTTGATGACTTTCATCTTTGCGCTTCTTTGCCG	910
QY	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA	182
Db	911	TGGAGATGGTGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAAAAGTTTACCTGGGAG	970
QY	182	spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA	202
Db	971	ACACTTGGAAACCGGCTTGACTTTTTCATCGTCAGGAGTGTCTGCGAGTACTCGCTGG	1030
QY	202	spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
Db	1031	ACCTGCAAAACGTTCAGCTTCTCAGCTGTTCAGGACAGTCCGTGTCTGCCACCGCTCAGGG	1090
QY	222	laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM	242
Db	1091	CCATTAAACGGGTGCCAGCATGCGCATCCTTGTACAGTTGTCTGCGATACGTTGCCCA	1150
QY	242	etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV	262
Db	1151	TGCTGGGCAACGTCTGTGCTGTCTGCTTCTTCGCTCTTCTTTCATCTTCGGCATCGTCGGCG	1210
QY	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP	282
Db	1211	TCCAGCTGTGGCAGGGCTGCTCGGAACCGATGCTTCCTACCTGAGAAATTCAGCCTCC	1270
QY	282	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI	302
Db	1271	CCCTGAGCGTGGACCTGGAGCGCTATTACCAGACAGAACGAGGATGAGAGCCCTTCA	1330
QY	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	1331	TCTGTCTCCACGCCACGGAGAACCGCATCGGTCTCTCAGAAAGCTGCCACGCTGCCGCG	1390
QY	322	lyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSera	342
Db	1391	GGGACGGGGCGGTGGCCCACTTTCGGGTCTGGACTATGAGGCCTACAACAGCTCCAGCA	1450
QY	342	snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP	362
Db	1451	ACACCACCTGTGTCAACTGGAACCACTACTACACCACTGCTCAGCGGGGAGACAAC	1510
QY	362	roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV	382
Db	1511	CCTTCAAGGGCGGCATCAACTTTGACAAACATTGGCTATGCTGGATCGCCATCTTCCAGG	1570
QY	382	allLeThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	1571	TCATCAGCTGGAGGCTGGTTCGACATCATGTACTTGTGATGGATGCTCATTCTTCT	1630
QY	402	yrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC	422
Db	1631	ACAAATTTCATCTACTTCATCTCTCATCATCTGGGCTCTTCTTTCATGATCAACCTGT	1690
QY	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	1691	GCCTGGTGGTGATTGCCACGAGTTCTCAGAGACCAAGCAGCGGGAAGCAGCTGATGC	1750
QY	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1751	GGGAGCAGCGTGTGCGGTTCTGTCCAACGCCAGCACCTGGCTAGCTTCTCTGAGCCCG	1810
QY	462	lySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
Db	1811	GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTACATCCTTCGTAAAGCAGCCCGCA	1870
QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1871	GGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGCGGTTGGGTGCTCAGCAGCCAGCAC	1930
QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1931	CCCTCGGGGCCAGGAGACCCAGCCAGCAGCTGCTCGTCTCCACCGCCGCTAT	1990
QY	522	erValHisHisLeuValHisHisHisHisHisHisTyrHisLeuGlyAsnG	542
Db	1991	CCGTCCACCACCTGGTGACCCACCACCACCACCATCACCACTACCACTCGGCAATG	2050
QY	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562
Db	2051	GGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGATGCCAATGGGTCCC	2110
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	2111	GCAGGCTCATGTGCCACCACCCCTCGACGCCTGCCCTTCCGGGGCCCCCCTGTGGCG	2170
QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2171	CAGAGTCTGTGCACAGCTTCTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2230
QY	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2231	CGCCCCCTCCAGGTCCCCATCTGAGGCATCCGGCAGGACTGTGGGCAGCGGGAAGGTGT	2290
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2291	ATCCCCACCGTGACACACAGCCCTCCACGGAGACGCTGAAGGAGAAGGCACCTAGTAGAGG	2350
QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2351	TGGCTGCCAGCTCTGGGCCCCCAACCTCTCACCGCCTCAACATFCCCACTCCCGGCCCTACA	2410
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2411	GCTCCATGCACAAGCTGTGGAGACACAGAGTACAGGTGCTTGCCTGCCAAAGCTCTTGCAAGA	2470
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2471	TCTCCAGCCCTTGTGTAAAGCAGACAGTGGAGCCTGTGGTCCACAGCTGCCCTTACT	2530
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2531	GTCCCCGGGCGGGCAGGGGAGGTGGAGCTCGCCGACCCGTGAATGCCTGACTCAGACA	2590
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2591	GCAGGCGAGTTTATGAGTTTACACAGGATGCCAGCACAGCGACCTCCGGGACCCCCACA	2650
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762

Db 2651 GC---CGGCGCAACGGAGCCTGGGCCAGATGCAGAGCCAGCTCTGTGCTGGCCTTCT 2707
QY 762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 2708 GGAGGCTAATCTGTGACACCTTCCGAAAGATTGTGGACAGCAAGTACTTTGGCCGGGAA 2767
QY 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db 2768 TCATGATCGCCATCCTGGTCAACACACTCAGCATGGGCATCGAATACCACGAGAGCCCG 2827
QY 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db 2828 AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTACCAGCCTCTTTGGCCCTGG 2887
QY 822 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db 2888 AGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTTGGCTACATCAAGAATCCCTACAACA 2947
QY 842 lePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyG 862
Db 2948 TCTTCGATGGTGTCTATTGGTTCATCAGCGTGTGGGAGATCGTGGCCAGCAGGGGGCGG 3007
QY 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
Db 3008 GCCTGTGCGTGTGCGGACCTTCCGCCGTGATGCGTGTGTAAGCTGGTGGCCTTCCTGC 3067
QY 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 3068 CGGCGCTGCAGCGGCAGCTGGTGTGCTCATGAAGACCATTGGAACCAACGTGGCCACCTTCT 3127
QY 902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 3128 GCATGCTGCTTATGCTCTTTCATCTTCATCTTCAGCATCTCGGCATGTCATCTCTTCGGCT 3187
QY 922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db 3188 GCAAGTTTGCCTCTGAGCGGGATGGGACACCCCTGCCAGACCGGAAGAAATTTTGACTCCT 3247
QY 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962
Db 3248 TGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTGACCCAGGAGGACTGGAAACAAAGTCC 3307
QY 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
Db 3308 TCTACAAATGGTATGGCCTCCACGTCGTCTGGCGGCCCTTATTTTCATTGCCCCTCATGA 3367
QY 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
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QY 1002 laGlu----- 1003
Db 3428 CGGAGGAATCAGCAAACGGGAAGATGCGAGTGGACAGTTAAGCTGTATTACAGTGCCTG 3487
QY 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db 3488 TCGACTCCAGGGGGGAGATGCCAACAAAGTCCGAATCAGAGCCCCGATTTCCTCACCCA 3547
QY 1019 erValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039
Db 3548 GCCTGGATGGTATGGGGACAGGAAGAAGTCTTGGCCCTTGGTGTCCCTGGGAGAGCACCC 3607
QY 1039 laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetS 1059
Db 3608 CGGAGCTGCGGAAGAGCCTGCTGCCGCTCTCATCATCCACACGCCGCCACACCCATGT 3667
QY 1059 erHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT 1079
Db 3668 CGTGCCCCAAGAGCACACGACCGGCGCTGGCGAGCGCTGGGCCCTGCGCTCGCGCCGCA 3727
QY 1079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProS 1099

Db 3728 CCAGCAGCAGCGGGTCCGCAGAGCCTGGGGCGGCC---CACGAGATGAAGTCACCGCCCA 3784
QY 1099 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1119
Db 3785 GCGCCCGCAGCTCTCCGCACAGCCCTTGAGCGCTGCAAGCAGCTGGACCAGCAGCGCT 3844
QY 1119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1139
Db 3845 CCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGAGAAGCCCAAGTGGAGAGC 3904
QY 1139 rgArgSerLeuLeuSerGlyGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG 1159
Db 3905 GCGCGTCCCTGTTGTCCGGAGAAAGGCCAGGAGAGCCAGGATGAAGAGGAGAGCTCAGAA 3964
QY 1159 luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1179
Db 3965 AGGAGCGGGCCAGCCCTCGGGCAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGGAGG 4024
QY 1179 laLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlas 1199
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QY 1199 erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1219
Db 4085 GTGGCCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAATGGCAAGTCGGCTTCAGGGCGCC 4144
QY 1219 euAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluG 1239
Db 4145 TGGCCCGGGCCCTGCGGCCCTGATGACCCCCCATCTGGATGGGGATGACGCCCGATGACGAGG 4204
QY 1239 lyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC 1259
Db 4205 GCAACTGAGCAAAAGGGGAACGGGTCCGCGGTGGATCCGAGCCCGACTCCCTGCGCTGCT 4264
QY 1259 ysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuL 1279
Db 4265 GCCTCAGCGAGACTCCTGGTCAGCCTACATCTTCCCTCCTCAGTCCAGGTTCCGCTCC 4324
QY 1279 euCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheL 1299
Db 4325 TGTGTACCCGGATCATCACCCACAAGATGTTCCGACCACGTGGTCTTGTGTATCATCTTCC 4384
QY 1299 euAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI 1319
Db 4385 TTAACATGCATCACCATCGCCATGGAGCGCCCCCAAATTGACCCCCACAGCGCTGAACGCA 4444
QY 1319 lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL 1339
Db 4445 TCITTCCTGACCCCTCTCCAATTACATCTTCACCGCAAGTCTTCTGGCTGAAATGACAGTGA 4504
QY 1339 ysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnV 1359
Db 4505 AGGTGGTGGCACTGGGCTGGTGTCTCGGGAGCAGCGTACCTCGGAGCAGTTGGAAACG 4564
QY 1359 alLeuAspGlyLeuLeuValIleSerValIleAspIleLeuValSerMetValSerA 1379
Db 4565 TGCTGGACGGGCTGTTGGTGTCTCATCTCCGTTCATCGACATTCGGTGTCCATGCTCTCTG 4624
QY 1379 spSerGlyThrLysIleLeuGlyMetLeuArgValIleuArgLeuLeuArgThrLeuArgP 1399
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QY 1399 roLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerS 1419
Db 4685 CGCTCAGGGTGTATCAGCCGGGGCCAGGGGCTGAAGCTGGTGGAGACGCTGATGTCTCT 4744
QY 1419 erLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyI 1439
Db 4745 CACTGAAACCCCATCGGCAACATGTAGTTCATCTGCTGTGCCTTCTTCATCATTTTCGGCA 4804
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Db 4805 TCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTTTTCGTGTGCCAGGGCGAGGATACCAGGA 4864

QY	1459	snIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrA	1479
DB	4865	ACATCACCAATAAATCGGACTGTCCGAGGCCAGTTACCGTGGTCCGGCACAAAGTACA	4924
QY	1479	snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyT	1499
DB	4925	ACTTTGACAACCTTGGCCAGGCCCTGATGTCCTGTTCGTTTGGCCTCCAAGGATGGTT	4984
QY	1499	rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetA	1519
DB	4985	GGGTGGACATCATGTACGATGGGCTGGTGTGGCGTGGACCCAGCAGCCCATCATGA	5044
QY	1519	snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV	1539
DB	5045	ACCACAAACCCCTGGATGCTGCTGACTTCATCTCGTTCCTGCTCATTTGTGGCCTTCTTTG	5104
QY	1539	alLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnG	1559
DB	5105	TCCTGAACATGTTGTGGGTGTGGTGGAGAACTTCCACAAGTGTCCGCAGCACCCAGG	5164
QY	1559	luGluGluGluAlaAargArgGluGluLysAargLeuArgLeuGluLysLysArgA	1579
DB	5165	AGGAAGAGGAGGCCGCGCGGGAGGAGAGAGCGCTACGAAGACTGGAGAAAAAGAGAA	5224
QY	1579	rgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA	1599
DB	5225	GGAGTAAGGAGAGCAGATGGCTGAAGCCCGAGTCAAAACCTTACTACTCCGACTACTCCC	5284
QY	1599	rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG	1619
DB	5285	GCTTCGGCTCCTCGTCCACCACCTTGTGCACCCAGCCACTACCTGGACCTCTTCATCACAG	5344
QY	1619	lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL	1639
DB	5345	GTGTCAATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCAGCAGCCCCAGATTTC	5404
QY	1639	euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV	1659
DB	5405	TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTCTTTGTCTTGAGTCTAG	5464
QY	1659	alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA	1679
DB	5465	TTTTTCAAACCTTGTGGCCTTTGGTTTCCGTCCGTTCTTCCAGGACAGGTGGAACCCAGCTGG	5524
QY	1679	spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL	1699
DB	5525	ACCTGGCCATTGTGCTGCTGTCCATCATTGGGCATCACGCTGGAGGAAATCGAGGTCAACG	5584
QY	1699	euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV	1719
DB	5585	CCTCGCTGCCCATCAACCCACCACCATCATCCGCATCATGAGGGTGTGCGCATTTGCCCCGAG	5644
QY	1719	alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA	1739
DB	5645	TGCTGAAGCTGCTGAAGATGCTGTGGGCATCGCGGCGCTGCTGGACACGGTGTGTCAGG	5704
QY	1739	laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759
DB	5705	CCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTGTGTGTTTTTCATCTTTGCAG	5764
QY	1759	laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL	1779
DB	5765	CTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCC	5824
QY	1779	euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS	1799
DB	5825	TGGGCGTTCATGCCACCTTTTCGAACTTTTGGCATGGCCCTTCTTAACCTCTTCCGAGTCT	5884
QY	1799	erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS	1819
DB	5885	CCACAGGTGACAAATTGGAATGGCAATTATGAAGGACACCCCTCCGGGACTGTGACCCAGGAGT	5944

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Db	5945	CCACCTGCTACAAACACGGTCACTCGCTATCTACTTTGTGTCTCTCGTCTGACGGCCC	6004
QY	1839	lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL	1859
Db	6005	AGTTCTGTGTAGTCAACGTGGTGATCGCGTGTCTGATGAAGCACCTGGAGGAGACA	6064
QY	1859	ysGluAlaIysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuS	1879
Db	6065	AGGAGGCCAAGAGGAGGCGGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCA	6124
QY	1879	erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA	1899
Db	6125	GCCCCCAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGGCCCTGGGTCGAGGGCCCCG	6184
QY	1899	snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS	1919
Db	6185	ACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCCT	6244
QY	1919	erGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProL	1939
Db	6245	CCCACTTTTCCCTGGAGCACCCCAACGATGCAGCCCCCACCCACGGAGCTGCCA-----	6297
QY	1939	euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA	1959
Db	6298	--GGACCAGACTTACTGACTGTGCGGAAGTCTGGGTCAGCCGAACGCACTCTCTGCCCA	6355
QY	1959	snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT	1979
Db	6356	ATGACAGCTACATGTGTGGCATGGGAGCACTGCCGAGGGCCCCCTGGGACACAGGGGCT	6415
QY	1979	rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT	1999
Db	6416	GGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCACGCCAGCAGATA	6475
QY	1999	hrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaP	2019
Db	6476	CCAGCTACATCTCGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCC	6535
QY	2019	roThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgP	2039
Db	6536	CAACCTGGGGCACCATCCCCAAACTGCCCCACAGGACGCTCCCTTTGGCTCAGAGGC	6595
QY	2039	roLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerA	2059
Db	6596	CACCTAGGGCGCCAGGAGCAATAAGACTGACTCCTTGGACGTTTCCGCGTCTGGGCTCAGAGGC	6655
QY	2059	rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerP	2079
Db	6656	GGGAAGACCTGCTGGCAGAGGTGAGTGGGGCCCTCCCCCGCCCTGGCCCCCTTACTCTT	6715
QY	2079	heTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL	2099
Db	6716	TCTGGGGCCAGTCAAGTACCCAGGCACAGAGCACTCCCGCAGCCACAGCAAGATCTCCA	6775
QY	2099	ysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp	2119
Db	6776	AGCACATGACCCCGCCAGCCCTTGCCAGGCCCAAGAACCCAACTGGGGCAAGGGCCCTC	6835
QY	2119	roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL	2139
Db	6836	CAGAGACCAGAAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCC	6895
QY	2139	eu---ProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerV	2158
Db	6896	TGCCCTCTGGCGCCAGGAGGAGCCCCCATCCCCACGGACCTGAAGAAGTGCTACAGCG	6955
QY	2158	alGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisS	2178
Db	6956	TGGAGGCCCCAGAGCTGCCAGGCGCCGCCCTACGTCCTGGCTGGATGAGCAGAGGAGACACT	7015
QY	2178	erIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerS	2198

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Db      7016 CTATCGCGTCAGTGCCTGGACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTA 7075
QY      2198 erLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProp 2218
Db      7076 ACCTTGGGGCCAGCCTCTTGGGGGGCCCCGGAGCCGGCCCAAGAAAACTCAGCCCGC 7135
QY      2218 roSerIleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyV 2238
Db      7136 CTAGTATCACCATAGACCCCCCGAGAGCCAAAGGTCCTCGGACCCCGCCAGCCCTGGTA 7195
QY      2238 alCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProL 2258
Db      7196 TCTGCCTCGGAGGAGGGCTCCGTCACGCGACTCCCAAGGATCCCTTGGCCTCTGGCCCCC 7255
QY      2258 euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuS 2278
Db      7256 CTGACAGCATGGCTGCCTCGCCCTCCCCAAAGAAAGATGTGCTGAGTCTCTCCGGTTAT 7315
QY      2278 erSerAspProThrAspMetAspPro 2286
Db      7316 CCTCTGACCCAGCAGACCTGGACCCC 7341
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RESULT 2
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

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Alignment Scores:
Pred. No.:      0      Length:      6822
Score:          10948.50      Matches:      2111
Percent Similarity: 94.03%      Conservative: 32
Best Local Similarity: 92.63%      Mismatches: 105
Query Match:      91.03%      Indels: 31
DB:                3      Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-426-998-3 (1-6822)

QY      34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db      2 TGGACGAGGAGGAGGATGGAGCGGGCCGAGGAGTCGGGACAGCCCCGGAGCTTCATGC 61
QY      54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspp 73
Db      62 GGCTCAACGACCTGTCGGGGGCGGGGGCCGGCCGGGGTCAGCAGAAAAAGGACC 121
QY      73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db      122 CGGGCAGCGCGGACTCCGAGGGCGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTTT 181
QY      93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db      182 TCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGCACGGTCTGTAACC 241
QY      113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
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QY      133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db      302 TCCGGCCATCGAGGACATCGCCTGTGACTCCCAGCGCTGCCGATCCTTGCAGCGCTTTG 361
QY      153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db      362 ATGACTTCATCTTTTGCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGCA 421
QY      173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db      422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
QY      193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db      482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCAGGA 541
QY      213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db      542 CAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACGGGTGCCCAGCATCGCATCCTTG 601
QY      233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db      602 TCACGTTGCTGTGGATACGCTGCCCATGCTGGGGAACGTCCTGCTGCTCTGCTTCTTCG 661
QY      253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db      662 TCTTCTTCATCTTCGGCATGCTCGGCGTCCAGCTGTTGGGCGGGCTGCTTCGGAACCGAT 721
QY      273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db      722 GCTTCTACCTGAGAAATTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAGA 781
QY      293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db      782 CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACCGGAGAACGGCATCGGT 841
QY      313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
Db      842 CCTGCAGAACGTCGCCACGCTGCGGGGACGGGGGGGGTGGCCCCACCTTGGGTCTGG 901
QY      333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
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QY      353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db      962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGCCATCAACTTTTGACAACATTG 1021
QY      373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db      1022 GCTATGCCTGGATCGCCATCTTCCAGGTCACTACGCTGAGGGGTGGGTGCGACATCATGT 1081
QY      393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV 413
Db      1082 ACTTTGTGATGGATGCTCATCTCTTCTACAATTTTCATCTACTTCTCCTCCTCATCATCG 1141
QY      413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db      1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGCTGGTGGTGAATTGCCACGCAGTTCTCAGAGA 1201
QY      433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas 453
Db      1202 CCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCCTGTCCAACGCCA 1261
QY      453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db      1262 GCACCTGGCTAGCTTCTCTGAGCCCGGCGAGCTGCTATGAGGAGCTGTCTCAAGTACCTGG 1321
QY      473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
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Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGTCCACCGCCGCTATCCGTCACACCTGGTGACACCCAGCCAGCCACC 1501
Qy 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACTACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGA 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT 573
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Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681
Qy 593 ysHisLeuGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCGCTGCCAGGCGGCCCTCCCAGGTCCCCATCTGAGGCATCCG 1741
Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGGACTGTGGGACGCGGAAGGTGTATCCACCGTGCAACCCAGCCCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
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Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert 673
Db 1862 GCCTCAACATCCCAACCGGGCCCTACAGTCCATGCACAAGTGTGTGAGACACAGAGTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
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Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGGTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGCAGGGAGGTGGAGTCCG 2041
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAAATGCCTGACTCAGACAGCGAGGAGTTATGAGTTTCAACAGGATGCC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
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Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
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Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
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Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACGAGCAGCCCGAGGAGCTTACCAAGCCCTAGAAATCAGCAACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
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Qy 1004 --- GlyAspAlaThrLysSerG 1010
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Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACACGGCCGCCACACCCATGTCTGTCGCCAAGAGCACACGCGGCTGGGCG 3178
Qy 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
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Qy 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
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Db 4016 AGCGGTACTGCGGAGCAGTTGGAACTGTGTGACGGGCTGTTGGTGTCTCATCTCCGTCA 4075
QY 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
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QY 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4136 TGCTGCGGTGCTGCGGACCCCTGCGCCGCTCAGGGTGATCAGCCGGCGCGGGGCTGA 4195
QY 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
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QY 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
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Db 4436 TGTTCTGTTTGGCCTCCAAGGATGGTTGGTGGACATCATGTACGATGGGCTGGATGCTG 4495
QY 1510 alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIles 1530
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QY 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
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Db 4676 GCCTACGAAGACTGGAGAAAAAGAGAGGAGTAAGGAGAAGCAGATGGCTGAAGCCAGT 4735
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Db 4736 GCAAAACCTTACTACTCCGACTACTCCCGCTTCCCGCTCTCGTCCACCACTTGTGCACCA 4795
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QY 1690 leThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgI 1710
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QY 1730 rgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuP 1750
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QY 1850 euMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaG 1870
Db 5516 TGATGAAGCACCTGGAGGAGAGCAACAAGGAGGCCCAAGGAGGAGGCCGAGCTAGAGGCTG 5575
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QY 1890 heLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProH 1910
Db 5636 TCCTCTGGCCTGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCCCTGGGGCTCTGC 5695
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Qy 2050 erLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProS 2070

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Qy 2169 heTrrpLeuAspGluGlnArgArgHisSerileAlaValSerCysLeuAspSerGlySerG 2189

Db 6467 CCTGGCTGGATGAGCAGAGAGACACTCTATCGCGTCACTGCTGCCTGGACAGCGGTCCC 6526

Qy 2189 lnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlys 2209

Db 6527 AACCCACCTGGGCACAGACCCCTCTAACCTTGGGGCCAGCCTCTTGGGGGCCCGGGA 6586

Qy 2209 erArgProLysLysLeuSerProProSerileSerileAspProProGluSerGlnG 2229

Db 6587 GCCGGCCCAAGAAAAACTCAGCCCGCTAGTATCACCATAGACCCCCCGAGAGCCCAAG 6646

Qy 2229 lySerArgProProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAsps 2249

Db 6647 GTCTCTGGACCCCGCCAGCCCTGGTATCTGTCTCCGGAGGAGGGCTCCGTCCAGCGACT 6706

Qy 2249 erLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysL 2269

Db 6707 CCAAGGATCCCTTGGCCTCTGGCCCCCTGTACAGCATGGTGCCTCGCCCTCCCCAAGA 6766

Qy 2269 ysAspThrLeuSerLeuSerGlyLeuSerSerSerProThrAspMetAspPro 2286

Db 6767 AAGATGTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGGACCCCC 6819

RESULT 3

US-09-949-016-3859

; Sequence 3859, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3859

; LENGTH: 7405

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-3859

Alignment Scores:

Pred. No.:	0	Length:	7405
Score:	10739.00	Matches:	2077
Percent Similarity:	92.09%	Conservative:	29
Best Local Similarity:	90.82%	Mismatches:	95
Query Match:	89.28%	Indels:	86
DB:	4	Gaps:	5

US-09-611-257A-24 (1-2287) x US-09-949-016-3859 (1-7405)

Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22

Db 281 CCGCCGGGGCCCCCGGTTGCGTGAGGACACCTCCTCTGAGGGCGCCGCTTGCCCTCT 340

Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTrrpThrArgArgMetGluArgAla 42

Db 341 CCGGATCGCCCGGGCCCCCGCTGGCCAGAGGATGGACGAGGAGGATGGAGCGGGCG 400

Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62

Db 401 CCGAGGAGTCGGGACAGCCCCGGAGCTTCATCGGGCTCAACGACCTGTCGGGGCGGGG 460

Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82

Db 461 GCCGGCCGGGGCGGGGTACAGAGAAAAGACCCGGGCAGCCGGAGCTCCGAGGGGAGG 520

Qy 82 lyLeuProTrrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102

Db 521 GGCTGCCGTACCCGGCGCTGGCCCCCGGTGGTTTCTTCTACTTGAGCCAGGACAGCCGCC 580

Qy 102 roArgSerTrrpCysLeuArgThrValCysAsnPro---TrrpPheGluArgValSerMetL 121

Db 581 CGCGGAGCTGGTGTCTCCGCACGGTCTGTAAACCCCTACCTGGTTTGAGCGCATCAGCATGT 640

Qy 121 euValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaC 141

Db 641 TGGTCATCCTTCTCAACTGCGTGACCTGGGCATGTTCCGGCCATGCGAGGACATCGCCT 700

Qy 141 ysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheA 161

Db 701 GTGACTCCAGCGCTGCCGGATCCTGAGGCCCTTGTGATGACTTCATCTTGGCTTCTTG 760

Qy 161 laValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuG 181

Db 761 CCGTGGAGATGGTGGTGAAGATGGTGGCTTTGGGCATCTTTGGGAAAAGTGTATTACCTGG 820

Qy 181 lyAspThrTrrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerL 201

Db 821 |||||GAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCGAGGGATGCTGGAGTACTCGC 880
QY 201 euAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuA 221
Db 881 TGGACCTGCAGAACGTCAGCTTCTCAGCTGTTCAGGACAGTCCGTGTGCTGCACCGCTCA 940
QY 221 rgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuLeuLeuP 241
Db 941 GGGCCATTAAACCGGTGCCAGCATGCGCATCCTTGTACAGTTGCTGTGCTGGATACGCTGC 1000
QY 241 roMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValG 261
Db 1001 CCATGCTGGGCAACGTCTGCTGCTCTGCTTCTTCGTCTTCTTCTATCTTCGGCATCGTCG 1060
QY 261 lyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerL 281
Db 1061 GCGTCCAGCTGTGGGCAGGGCTGCTTCGGAACCGATGCTTCTTACCTGAGAAATTCAGCC 1120
QY 281 euProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProp 301
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QY 301 heIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuA 321
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QY 341 erAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisA 361
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QY 361 snProPheIysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheG 381
Db 1361 ACCCTTCAAGGGCGCCATCAACTTGACAACATTGGGTATGCTGGATCGCATCTTCC 1420
QY 381 lnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerP 401
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QY 401 heTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnL 421
Db 1481 TCTACAAATTTCATCTACTTCTATCTCTCATCATCGTGGGTCTCTTCTTCATGATCAACC 1540
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Db 1541 TGTGCCTGTGTGTGATTGCCACGCAGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGA 1600
QY 441 etArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluP 461
Db 1601 TGCGGGAGCAGCTGTGCGGTTCTGTCCAACGCCAGCACCTGGCTAGCTTCTCTGAGC 1660
QY 461 roGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaA 481
Db 1661 CCGGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTACATCCTTCTGTAAGGCAGCCC 1720
QY 481 rgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProv 501
Db 1721 GCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGCGGGTTGGGTGCTCAGCAGCCAG 1780
QY 501 alAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgL 521
Db 1781 CACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCTGCTCTCGCTCCCAACCGCCGCC 1840
QY 521 euSerValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuGlyA 541
Db 1841 TATCCGTCCACCACCTGGTGCACCACCACCACCACCATCACCACCATCACCCTGGGCA 1900
QY 541 snGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlyS 561
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Db 1901 ATGGGACGCTCAGGGCCCCCGGGCCAGCCCCGGAGATCCAGGACAGGGATGCCAATGGGT 1960
QY 561 eArArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg 581
Db 1961 CCGCCGGCTCATGTGCACACCAACCTCGACGCCTGCCCTCTCCGGGGCCCCCCTGGTG 2020
QY 581 lyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysG 601
Db 2021 GCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCC 2080
QY 601 lnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysV 621
Db 2081 AGCGCCCCCTCCCAGGTCCCCATCTGAGGCATCCGGCAGGACTGTGGGCAGCGGAAGG 2140
QY 621 alTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValG 641
Db 2141 TGTATCCACCGTGCACACAGCCCTCCACCGGAGACGCTGAAGGAGAGGCACTAGTAG 2200
QY 641 luValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProp 661
Db 2201 AGGTGGCTGCCAGTCTGGGCCCCCAACCCCTCACAGCCTCAACATCCCAACCCGGGCCCT 2260
QY 661 heSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysL 681
Db 2261 ACAGTCCATGCACAAGCTGCTGGAGACACAGAGTACAGGTGCCTGCCAAAGTCTTGCA 2320
QY 681 ysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProt 701
Db 2321 AGATCTCCAGCCCTTGTGTGAAAGCAGACAGTGGAGCCTGTGTTCCAGACAGTGCCCT 2380
QY 701 yrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSera 721
Db 2381 ACTGTCCCCGGGCGGGGAGGGAGGTGGAGTCCGCCGACCGTGAAATGCTGACTCAG 2440
QY 721 spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH 741
Db 2441 ACAGCAGGCAGTTTATGAGTTCACACAGGATGCCAGCAGCAGCACGACCTCCGGACCCCC 2500
QY 741 isSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaP 761
Db 2501 ACAGC--CGGCGGCAACGGAGCCTGGGCCAGATGCAGAGCCCAGCTCTGTGTGGCCT 2557
QY 761 heTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgG 781
Db 2558 TCTGAGGCTAATCTGTGCACACCTTCCGAAAGATTGTGGACAGCAAGTACTTTGGCCGG 2617
QY 781 lyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnP 801
Db 2618 GAATCATGATCGCCATCCTGGTCAACACACTCAGCATGGGCATCGAATACCACGAGCAGC 2677
QY 801 roGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaL 821
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QY 821 euGluMetLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrA 841
Db 2738 TGGAGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTGGCTACATCAAGAATCCCTACA 2797
QY 841 snIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG 861
Db 2798 ACATCTTCGATGGTGTCAATTGTGTTCATCAGCGTGTGGAGATCGTGGGCCAGCAGGGGG 2857
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QY 921 lYcysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsps 941
Db 3038 GCTGCAAGTTTGCCTCTGAGCGGATGGGACACCTCGCCAGACCGGAAGATTTTGACT 3097
QY 941 erLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysV 961
Db 3098 CCTTGCTCTGGGCCATCGTCACTGTCTTCAGATCCTGACCCAGGAGACTGGAACAAAG 3157
QY 961 alLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuM 981
Db 3158 TCCTCTACAATGGTATGGCCTCCACGTCGTCGGGGGGCCCTTATTTCAATTGCCCTCA 3217
QY 981 etThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheG 1001
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QY 1001 lnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPheSerProSerVala 1021
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Db 3338 ATGGTATGGGACAGGAAGAAGTGTGGCCTTGGTGTCCCTGGGAGAGCACCCGGAGC 3397
QY 1041 euArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisP 1061
Db 3398 TGGGAAGAGCCTGCTGCCGCTCTCATCATCACACGGCCGCCACCCATGTCGCTGC 3457
QY 1061 roLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSers 1081
Db 3458 CCAAGAGACCAAGCAGCGCCTGGGCGAGGGCGCTGGGCCCTGCGTCGCGCCGCACCAGCA 3517
QY 1081 erSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaA 1101
Db 3518 GCAGCGGCTCGCAGAGAGCCTGGGGCGGCC---CACGAGATGAAGTACCGCCCGAGCGCCC 3574
QY 1101 rgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSera 1121
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QY 1121 rgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgS 1141
Db 3635 GGAACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGAGAAGCCCAAGTGAGAGCGCGGT 3694
QY 1141 erLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspA 1161
Db 3695 CCCTGTGTCTGGGAGAGGCCAGGAGAGCCAGGATGAAGAGGAGAGCTCACAAGAGGAGC 3754
QY 1161 rgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysS 1181
Db 3755 GGGCCAGCCCTGCGGGCAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGA 3814
QY 1181 erSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyA 1201
Db 3815 GTTCTTTGACCTGCCAGACACACTGCAGGTGCCAGGCTGCATCGCACTGCCAGTGGCC 3874
QY 1201 rgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaA 1221
Db 3875 GAGGGTCTGCTTCTGAGCACCAAGACTGCAATGGCAAGTGGCTTCAGGGCGCCTGGCCC 3934
QY 1221 rgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnL 1241
Db 3935 GGGCCCTGCGGCTGATGACCCCCCACTGGATGGGATGACGCCGATGACGAGGGCAACC 3994
QY 1241 euSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysArgG 1261
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QY 1261 luArgAspSerTrpSerAlaTyriIlePheProProGlnSerArgPheArgLeuLeuCysH 1281
Db 4055 AGCGAGACTCCTGGTCAGCCTACATCTTCCCTCCTCAGTCCAGGTTCCGCGCTCCTGTGTC 4114

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QY 1301 ysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheL 1321
Db 4175 GCATACCATCGCCATGGAGCGCCCCAAATTTGACCCCCACAGCGCTGAACGCATCTTC 4234
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QY 1341 alAlaLeuGlyTrpCysPheGlyGluGlnAlaTyriLeuArgSerSerTrpAsnValLeuA 1361
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QY 1361 spGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerG 1381
Db 4355 ACGGGCTGTGGTGTCTCATCTCCGTTCATCGACATTCTGGTGTCCATGGTCTCTGACAGCG 4414
QY 1381 lyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuA 1401
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Db 4475 GGGTGATCAGCCGGCGCAGGGGCTGAAGCTGGTGTGGAGACGCTGATGTCTCACTGA 4534
QY 1421 ysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuG 1441
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QY 1441 lyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleT 1461
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QY 1461 hrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheA 1481
Db 4655 CCAATAAATCGGACTGTGCCGAGGCCAGTTACCGGTGGTCCGGCACAAAGTACAACTTTG 4714
QY 1481 spAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVala 1501
Db 4715 ACAACCTTGGCCAGGCCCTGATGTCCCTGTTCGTTTTTGGCCTCCAAGGATGGTTGGTGG 4774
QY 1501 spIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisA 1521
Db 4775 ACATCATGTACGATGGCTGGATGCTGTGGCGCTGGACCCAGCAGCCCATCATGAACCA 4834
QY 1521 snProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuA 1541
Db 4835 ACCCTGGATGCTGTACTTTCATCTCGTCTCTGCTCATTTGGCTTCTTTGTCTCTGA 4894
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QY 1581 ysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheA 1601
Db 5015 AGGAGAAGCAGATGGCTGAAGCCCGAGTGCAGAAACCTTACTACTCCGACTACTCCCGCTTCC 5074
QY 1601 rgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValI 1621
Db 5075 GGCTCCTCGTCCACCACTGTGCACCGACCACTACCTTCTTGACCTCTTTCATCACAGGTGTCA 5134
QY 1621 leGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspG 1641
Db 5135 TCGGGCTGAACGTGGTCACCATGGCCATGGAGCACTACCAGAGCCCGCAGATTCTGGATG 5194
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QY 1661 ysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuA 1681
Db 5255 AACTTGTGGCCTTTGGTTTCCGTCGGTTCTTCCAGGACAGGTGGAAACGAGCTGGACCTGG 5314
QY 1681 laileValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerL 1701
Db 5315 CCATTGTGCTGTCTCCATCATGGGCATCACGCTGGAGAAATCGAGGTCAACGCCTCGC 5374
QY 1701 euProfileAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuL 1721
Db 5375 TGCCCATCAACCCACCACCATCATCGGCATCATGAGGTGCTGCGCATTTGCCGAGTGTGA 5434
QY 1721 ysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuP 1741
Db 5435 AGCTGCTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACGGTGATGCAGGCCCTGC 5494
QY 1741 roGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuG 1761
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QY 1801 lyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrC 1821
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QY 1821 ysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheV 1841
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QY 1881 lnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerT 1901
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QY 1901 hrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyP 1921
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Db 6035 TTTCCCTGGAGCACCCACGATGACAGCCCCACCCACCGAGCTGCCA-----GGAC 6085
QY 1941 roAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspS 1961
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QY 1961 erTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyL 1981
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QY 1981 euProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerC 2001
Db 6206 TCCCCAAAGCTCAGTCAGGCTCCGCTTGTCCGTTTCACTCCAGCCAGCAGATACCAGCT 6265
QY 2001 ysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrT 2021

Db 6266 ACATCTCTGCAGTTCCCAAAGATGCACCTCATCTGTCTCCAGCCCCACAGCGCCCCAACCT 6325
QY 2021 rpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuA 2041
Db 6326 GGGGCACCATCCCCAAACTGCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGCCACTCA 6385
QY 2041 rgArgGlnAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluA 2061
Db 6386 GGGCCAGGCAGCAATAAGACTGACTCCTTGGACCTTCAGGCTTGGGCAGCGGGGAG 6445
QY 2061 spLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpG 2081
Db 6446 ACCTGCTGGCAGAG----- 6459
QY 2081 lyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisI 2101
Db 6459 ----- 6459
QY 2101 leArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluT 2121
Db 6459 ----- 6459
QY 2121 hrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPros 2141
Db 6459 ----- 6459
QY 2141 erSerGlnGluGluProLeuPheProArgAspLeuLysCysTyrSerValGluThrG 2161
Db 6460 -----GAGGAGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGCC 6511
QY 2161 lnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaV 2181
Db 6512 AGAGTGCACGCGCGGCCACGCTCCTGGCTGGATGAGCAGAGGACACTCTATCGCCG 6571
QY 2181 alSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyG 2201
Db 6572 TCAGTGCCTGGACAGCGGCTCCCAACCCCACTGGGCACAGACCCCTCTAACCTTGGGG 6631
QY 2201 lyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIles 2221
Db 6632 GCCAGCCTCTTGGGGGCTGGGAGCGCGGCCCAAGAAAAAACTCAGCCCGCTAGTATCA 6691
QY 2221 erIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuA 2241
Db 6692 CCATAGACCCCCCGAGAGCAAGGTCTCTCGGACCCCGCCAGCCCTGGTATCTGCCTCC 6751
QY 2241 rgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSerT 2261
Db 6752 GGAGAGGGTCCGCTCCAGCGACTCCAAGGATCCCTTGGCCTCTGGCCCCCTGACAGCA 6811
QY 2261 hrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspP 2281
Db 6812 TGGCTGCCTCGCCCTCCCAAGAAAGATGTGTGAGTCTCTCCGGTTTATCTCTGACC 6871
QY 2281 roThrAspMetAspPro 2286
Db 6872 CAGCAGACTGGACCCC 6888

RESULT 4

US-08-984-709A-49
; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla

STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 249...7307
OTHER INFORMATION:
US-08-984-709A-49

Alignment Scores:					
Pred. No.:	0	Length:	7898		
Score:	6241.00	Matches:	1385		
Percent Similarity:	64.96%	Conservative:	209		
Best Local Similarity:	56.44%	Mismatches:	537		
Query Match:	51.89%	Indels:	325		
DB:	3	Gaps:	64		

US-09-611-257A-24 (1-2287) x US-08-984-709A-49 (1-7898)					
QY	3	ProHisArgValProArgCysValArgThrProLeuArgGlySerAlaArgProSer	22		
Db	188	CCCGGGCATCCCCGCCGGACCGCCGCCGCAGACGAGGTGCTGC-CGGCCG---	243		
QY	23	SerAspProProGlyProArgLeuAlaArgGly-----Trrp	34		
Db	244	-----CCACCATGCCAGG--GCGCACGGCCCGACGAGGTCCGGGTGCCCTGG	294		
QY	35	ThrArgArg-----ArgMetGluArgAlaProArgSer	45		
Db	295	GCGCGCCGCCCTTGCCCTTGGCGGTGGTGGGGCGTCCTCCCGAGAGCCCCCGGGCGC	354		
QY	46	ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly	65		
Db	355	CGGGACGCGAGCGGAGCGGGGTCCGAGCTCGGCGTGTCACTCCGAGAGCCCG-GCG	413		
QY	66	AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr	85		
Db	414	GCC-----GAGCGCGCGCGGAGCTGGGTGCCGACGAGGAGCGCGTCCCCTAC	464		
QY	86	ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp	105		
Db	465	CCGGCCTTGGCGGCCACGGTCTTCTTCTGCTCGGTCCAGACCACGCGGCCCGCAGCTGG	524		
QY	106	CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu	125		
Db	525	TGCTCTCCGGCTGGTCTGCAACCCCATGGTTTCGAGCACGTGAGCATGTGGTAATCATGCTC	584		

QY	126	AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145
Db	585	AACTGCGTGACCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGGGCTCCGAGCGC	644
QY	146	CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal	165
Db	645	TGCAACATCTGGAGGCTTGGGCTTACGCCCTTCATTTTCGCTTTTTCGCGTGGAGATGGTC	704
QY	166	ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn	185
Db	705	ATCAAGATGGTGGCTTGGGCTTTCGGGCAGAAAGTGTACCTGGGTGACACGTGGAAC	764
QY	186	ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn	205
Db	765	AGGCTGGATTCTTCATCGTGGCGGGCATGATGGAGTACTCGTTGGACGGACACAAC	824
QY	206	ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg	225
Db	825	GTGAGCCTCTCGGCTATCAGGACCGTGGGGTGTCTGGGCCCTCCGGCCCATCAACCGC	884
QY	226	ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn	245
Db	885	GTGCCTAGCATCGGATCCTGGTCACTCTGCTGTGGATACGCTGCCCCATGCTCGGGAAC	944
QY	246	ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp	265
Db	945	GTCCCTTCTGTGCTTCTTCGCTCTTCTTCATTTTCGGCATCGTTGGCGTCCAGCTCTGG	1004
QY	266	AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal	285
Db	1005	GCTGGCCTCCTGGGAACCGCTGCTTCTCGACAGTGCCTTTGTTCAGGAACAACAACCTG	1064
QY	286	Asp---LeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSer	304
Db	1065	ACCTTCTCGGCGGTACTACAGACGGAGAGGGCGAGGAGAACCGTTTCATCTGCTCC	1124
QY	305	GlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly	324
Db	1125	TCAGCGGAGACACCGCATGCAGAAAGTGTCTGCACATCCCC-----GGCCGCCGC	1175
QY	325	GlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsn-----	338
Db	1176	GAGCTGGCATGCCCCCTGCACCCCTGGCTGGGAGGCCCTACCGCAGCCGCGAGGGG	1235
QY	339	--SerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla	357
Db	1236	GTGGCGCTGCACGCAACGCTGCATCAACTGGAACCACTACACACGTGCGCGCTCG	1295
QY	358	GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle	377
Db	1296	GGTGACTCCAACCCCCACAACGGTGCCATCAACTCGACAACATCGGCTACGCTGGATT	1355
QY	378	AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp	397
Db	1356	GCCATCTTCAGGTGATCAGCTGGAAGGCTGGGTGGACATCATGTACTACGTATGGAC	1415
QY	398	AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe	417
Db	1416	GCCCCACTCATTCACAACTTCATCTATTTCATCTGCTCATCATCGTGGGCTCTTCTTC	1475
QY	418	MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu	437
Db	1476	ATGATCAACCTGTGCCCTGGTGGTGATTGCCACGCACTCTCGGAGACGAAGACGGGAG	1535
QY	438	SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer	457
Db	1536	AGTCAGCTGATGCGGAGCAGCGGCGCACGCCACCTGTCCAACGACAGCACGCTGGCCAGC	1595
QY	458	PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg	477
Db	1596	TTCTCCGAGCTGGCAGCTGCTACGAAGAGCTGCTGAAGTACGTGGGCCACATATTCCGC	1655

QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1656 AAGGTCAAGCGCGCAGCTTGCCTCTACGCCCTGGCAGAGCCGCTGGCGCAAGAAG 1715
QY 498 SerSerProValAlaAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1716 GTGACCCCGAGTGCTGTGCAAGCGCCAGGGTCCC-----GGG 1751
QY 518 HisArgArg-----LeuSerValHisHisLeuVal---HisHis 529
Db 1752 CACCGCCAGCGCGGCAGGCAGGCACACAGCCTCGGTGCACCACCTGGTCTACCACCAC 1811
QY 530 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAla 549
Db 1812 CATCACCAACCACCACCACTACCATTTTCAGCCATGGCAGCCCCCGCAGGCCCGCCCC 1871
QY 550 SerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu-----Pro 567
Db 1872 GAGCCAGGCGCTGCGAC-----ACCAGGCTGGTCCGAGTGCGCGC 1913
QY 568 ProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSer 587
Db 1914 CCCCCCTCGCACACTTCCCCAGGCGCGGACCCCC---GACGCAGAGTCTGTGCACAGC 1970
QY 588 PheTyrHisAlaAspCysHisLeuGlu-----ProValArgCysGlnAlaProProPro 605
Db 1971 ATCTACCATGCCGACTGCCACATAGAGGGCGCGCAGGAGGGCCCCGGTGGCACATGCC 2030
QY 606 ArgCysProSerGluAlaSerGlyArg---ThrValGlySerGlyLysVal---TyrPro 623
Db 2031 GCAGCCACTGCGGCTGCCAGCCTCAGGCTGGCCACAGGGTGGCACCATGAACACTACCC 2090
QY 624 ThrVal-----HisThrSerProProProGluIle 633
Db 2091 ACGATCTGCCCTCAGGGGTGGGAGCGGCAAGGCAGCACCGCCCCGGACCCCAAG--- 2147
QY 634 LeuLysAspLysAlaLeuValGluValAlaProSerPro-----Gly 647
Db 2148 -----GGGAAGTGGGCGGTGGACCGCGCAGGCACCGGGGGCACGGC 2189
QY 648 ProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMethHisLysLeu 667
Db 2190 CCGTTGAGCTGAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTG 2237
QY 668 LeuGluThrGlnSerThrGlyAlaCys-----HisSerSer-----Cys 680
Db 2238 GTCGGGGAGCATGGACTGGGCCAGGCCCTGGCCATCTGTGGGCCTCAGTGTGCCCTGC 2297
QY 681 LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
Db 2298 CCCCTGCCAGCCCC-----CCAGCGGGCACACTGACCTGTGAGCTGAAGAGTGCCTG 2351
QY 701 TyrCysAlaArgThr---GlyAlaGlyGluProGluSerAlaAspHisValMetProAsp 719
Db 2352 TACTGCACCGTGCCTGGAGGACCGGAGGTGAGCTCAGCGGCTCGGAAAGTGGAGAC 2411
QY 720 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 739
Db 2412 TCAGATGGCGGTGGCGTCTATGAATTACGCAGGACGTCGGGCACGGTGACCGGTGGGAC 2471
QY 740 Pro-----HisSerArg 743
Db 2472 CCCACGGACCAACCCCGTGCAGCGGACACACCAGGCCCCAGGCCAGCCCCAGCGG 2531
QY 744 ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArg 763
Db 2532 CGGGCACAGCAGAGGGCAGCCCCG---GGCGAGCCAGGCTGGATGGGCGCCTCTGGGTT 2588
QY 764 LeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMet 783
Db 2589 ACCTTACGGGCAAGCTGCGCCGCATCGTGGACAGCAAGTACTTCAGCCGTGGCATCATG 2648
QY 784 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGlu 803

Db 2649 ATGGCCATCCTTGTCAACACCGCTGAGCATGGCGCTGGAGTACCATGAGCAGCCCGAGGAG 2708
QY 804 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 823
Db 2709 CTGACTAATGCTCTGGAGATCAGCAACATCGTGTTCACAGCATGTTTGCCTGGAGATG 2768
QY 824 LeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 843
Db 2769 CTGCTGAAGCTGTGGCCTGCGGCCCTCTTGGGCTACATCCGGAACCCGTAACATCTTC 2828
QY 844 AspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyGlyGlyLeu 863
Db 2829 GACGCGCATCATCGTGGTTCATCAGCGTCTGGAGATCGTGGGGCAGGCGGCGTGGCTTG 2888
QY 864 SerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAla 883
Db 2889 TCTGTGCTGCGCACCTTCCGGCTGCTGCGTGTGCTGAAGCTGGTGGCTTCTGCCAGCC 2948
QY 884 LeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMet 903
Db 2949 CTGGCGGCCAGCTCGTGGTGTGGTGAAGACCATGGACAACGTGGCTTACCTTCTGCACG 3008
QY 904 LeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLys 923
Db 3009 CTGCTCATGCTCTTCAATTTTCATCTTCAGCATCCTGGGCATGCACCTTTTCGGCTGCAAG 3068
QY 924 PheAlaSerGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeu 942
Db 3069 TTCAGCCTGAAGACAGACACCGGAGACACCGTGCCTGACAGGAAGAACTTCGACTCCCTG 3128
QY 943 LeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeu 962
Db 3129 CTGTGGGCCATCGTCACCGTGTTCAGATCCTGACCCAGGAGGACTGGAACGTGCTCTG 3188
QY 963 TyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThr 982
Db 3189 TACACGGCATGGCCTCCACCTCCTCTCTGGCGCGCCTCTACTTCTGTGGCCCTCATGACC 3248
QY 983 PheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAla 1002
Db 3249 TTCGGAACATATGTGCTCTTCAACCTGTGTGGTGGCCATCCTCGTGGAGGGCTTCCAGGCG 3308
QY 1003 GluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspGly 1022
Db 3309 GAGGCGATGCCAACAGATCCGACACGACGAGCAGGACAAGACGTCGGTCCACTTCGAGGAG 3368
QY 1023 AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeu----- 1035
Db 3369 GACTTCCACAAGCTCAGAGAATCCAGACCACAGAGCTGAAGATGTGTTCCTGGCCGTG 3428
QY 1036 -----GlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThr 1053
Db 3429 ACCCCCAACGGGCACCTGGAGGACGAGGCAGCCTTCCCCTCCCTCATCATGTGCACA 3488
QY 1054 AlaAlaThrProMetSerHisProLysSerSerSerSer---ThrGlyValGlyGluAlaLeu 1072
Db 3489 GCTGCCACGCCCATGCCTACCCCAAGAGCTCACCATTCCTGGATGCAGCCCCCAGCCTC 3548
QY 1073 GlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHis 1092
Db 3549 CCAGACTCTCGCGTGGCAGCAGCAGCTCCGGGACCCGCCACTGGGA----- 3596
QY 1093 GluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSer 1112
Db 3597 GACCAGAAGCCTCCGGCCAGCCTCCGAAGTTCTCCCTGTGCCCTTGGGCCCCCAGTGGC 3656
QY 1113 SerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArg 1132
Db 3657 GCCTGGAGCAGCCGGCGCTCCAGCTGGAGCAGCCTGGGCGCGTGGCCCCCAGCCTCAAGCGC 3716
QY 1133 ArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAsp 1152

Db 3717 CGCGCCAGTGTGGGAAACGTGAGTCCCTGCTGTCTGGCGAGGGCAAGGGCAGCCGAC 3776
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QY 1171 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu--- 1189
Db 3831 CGGGCCGAGTCCCTGGACCCACGGCCCTGCGCGCGCGCCCTCCCGCTACCAAGTGC 3890
QY 1190 -----GlnValProGlyLeuHis-----ArgThrAlaSer 1199
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QY 1200 GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3951 CACCGTGAGGATGCAGCCGAGCTTGACGACGACTCGGAGGACAGCTGCTCCGCGCTG 4010
QY 1220 AlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGly 1239
Db 4011 CATAAAGTGTGGAGCCCTACAAGCCCCAG----- 4040
QY 1240 AsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCys 1259
Db 4041 -----TGG-----TGC 4046
QY 1260 ArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeu 1279
Db 4047 CGGAGCGCGAGGCTGGGCCCTCTACCTCTTCTCCCCACAGAACCGGTTCGCGTCTCC 4106
QY 1280 CysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeu 1299
Db 4107 TGCCAGAAGGTCAACACACAAGATGTTTGATCACGTGGTCTCTCGTCTTCATCTTCTC 4166
QY 1300 AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1319
Db 4167 AACTGGTCAACCATCGCCCTGGAGAGGCTGACATTGACCCCGGACGACCGAGCGGTC 4226
QY 1320 PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys 1339
Db 4227 TTCCTCAGCGTCTCCAATACATCTTCACGGCCATCTTCGTGGCGGAGATGATGGTGAAG 4286
QY 1340 ValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnVal 1359
Db 4287 GTGGTGGCCCTGGGCTGCTGCCGCGAGCACGCTACCTGCAGAGCAGCTGGAACCTG 4346
QY 1360 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsp 1379
Db 4347 CTGGATGGGCTGCTGGTGTCCCTGGTGGACATTGCTGGGCCATGGCCTCGGCT 4406
QY 1380 SerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPro 1399
Db 4407 GGTGGCGCAAGATCCTGGGTGTCTGCGGTGCTGCTGCTGCGGACCTGCGGCCT 4466
QY 1400 LeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSer 1419
Db 4467 CTAAGGGTCAACCGCGGCCCGGGCCTCAAGCTGGTGGTGGAGACGCTGATATCGTGC 4526
QY 1420 LeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIle 1439
Db 4527 CTCAGGCCCATTGGGAACATCGTCTCATCTGCTGCGCCTCTTCATCATTTTGGGCATC 4586
QY 1440 LeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsn 1459
Db 4587 TTGGGTGTGAGCTCTTCAAAGGGAAGTTCTACTACTGCGAGGCGCCCGACACGAGAAC 4646
QY 1460 IleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsn 1479
Db 4647 ATCTCCACCAAGGCACAGTCCCGGGCGCCCACTACCGCTGGGTGCGACGCAAGTACAAC 4706
QY 1480 PheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrp 1499
Db 4707 TTCGACAACCTGGCCAGGCCCTGATGTCGTGTTCTGCTGTCTCATCCAAGGATGGATGG 4766

QY 1500 ValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsn 1519
Db 4767 GTGAACATCATGTACACGGGCTGGATGCCGTGGGTGTCGACCAGACGCTGTGCAGAAC 4826
QY 1520 HisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheVal 1539
Db 4827 CACAACCCCTGGATGCTGTACTTTCATCTCTCTCTCTCATCTGCTCATCTGCTTCTTCTG 4886
QY 1540 LeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGlu 1559
Db 4887 CTCAACATGTTCTGGGCTGCTGGTCGAGAACTCCACAAGTCCCGCAGCACCCAGGAG 4946
QY 1560 GluGluGluAlaArgArgGluGluLysArgLeuArgLeuGluLysLysArgArg 1579
Db 4947 GCGGAGGAGCGCGCGGAGAGGAGAGCGGCTGCGGCGCCTAGAGAGGAGCGCAGG 5006
QY 1580 SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1599
Db 5007 AGCACTTTCGCCAGC--CCAGAGGCCCGCGCGGCCCTACTATGCCGACTACTCGCCC 5063
QY 1600 PheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGly 1619
Db 5064 ACGGCGCGCTCCATTCACCTCGCTGTGCACCGCCACTATCTCGACCTCTTTCATCACCTTC 5123
QY 1620 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1639
Db 5124 ATCATCTGTGTCAACGTCACTACCATGTCCATGGAGCACTATAACCAACCCCAAGTCGCTG 5183
QY 1640 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal 1659
Db 5184 GACGAGGCCCTCAAGTACTGCAACTACGTCTTCACCATCGTGTTCCTTCGAGGCTGCA 5243
QY 1660 PheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAsp 1679
Db 5244 CTGAAGCTGTGTAGCATTTGGGTTCGCTCGTTCCTTCAAGACAGGTGGAACACAGCTGGAC 5303
QY 1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699
Db 5304 CTGGCCATCGTGTCTGTCACTCATGGGCATCACGCTGGAGGAGATAGAGATGAGCGCC 5363
QY 1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719
Db 5364 GCGCTGCCCATCAACCCCAACCATCATCCGATCATGCGGTGCTTCGATTCGCCGTGTG 5423
QY 1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739
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QY 1740 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAla 1759
Db 5484 CTCGCCCAAGTGGGAACTTGGGCCCTTCTTTCATGCTCTCTTTTATCTATGCTGCG 5543
QY 1760 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1779
Db 5544 CTGGAGTGGAGCTGTTGGGAGGCTGGAGTGCAGTGAAGACAACCCCTGCGAGGCGCTG 5603
QY 1780 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1799
Db 5604 AGCAGGCACGCCACCTTCAGCAACTTCGGCATGGCCTTCCTCAGCTGTTCCGCGTGTCC 5663
QY 1800 ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys-----Asp 1816
Db 5664 ACGGGGACAACTGGAACGGGATCATGAAGACACGCTGCGCGAGTGTCCCGTGAGGAC 5723
QY 1817 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1836
Db 5724 AAGCACTGCCCTGAGCTACCTGCCGCCCTGTGCGCCCTCTACTTCGTGACCTTCGTGCTG 5783
QY 1837 ThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGlu 1856
Db 5784 GTGGCCCAAGTTCGTGTGTGTGAACGTGGTGGTGGCGCTGTCTCATGAAGCACCTGGAGGAG 5843


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QY 1857 SerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuMetLys 1876
Db 5844 AGCAACAAGGAGGCACGGAGGATCGGAGTCGGACGCGAGATCGAGCTGGAGATGGCG 5903
QY 1877 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlu 1896
Db 5904 -----CAGGCGCCCGGG 5915
QY 1897 GlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly 1916
Db 5916 AGTGCACGCGGGTGGACCGCGACAGGCCT----- 5945
QY 1917 AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluValPro 1936
Db 5946 -----CCCTTGCCCGCAGGAGTCCG 5966
QY 1937 ValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer 1956
Db 5967 GCGGCCAGGATGCCCAACCTGGTTGCACGCAAGGTGTCCGTGTCCAGGATGCTCTCG 6026
QY 1957 LeuProAsnAspSerTyrMetCysArgAsnGlySerThrAla----- 1970
Db 6027 CTGCCCAACGACAGCTACATGTTCCAGGCCCGTGGTGCCTGCCTCGGCGCCCCACCCCGCG 6086
QY 1971 -----GluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1987
Db 6087 CCGCTGCAGAGGTGGAGATGGAGACCTATGGGCGCGGACCCCT-----TTGGGC 6137
QY 1988 SerIleLeuSerValHisSerGlnProAlaAlaAspThrSerCysIleLeuGlnLeuProLys 2007
Db 6138 TCCGTTGCCTCTGTGCACCTCTCCGCCCGCAGAGTCCTGTGCCTCCCTCCAGATCCCACTG 6197
QY 2008 AspValHis-----TyrLeuLeuGlnProHisGlyAla 2018
Db 6198 GCTGTGTCTCTCCAGCCAGGAGCGCGGAGCCCTCCAGCCCTGTCTCCCTCGGGGCACA 6257
QY 2019 ProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2038
Db 6258 -----GCCGCTCCCCCAGTCTCAGCCGG 6281
QY 2039 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2058
Db 6282 CTGCTCTGCAGACAGGAGGCTGTGCACACCGATTCTCTGGAAGGAAG---ATTGACAGC 6338
QY 2059 ArgGluAspLeuLeuSerGluVal-----SerGlyProSerCysProLeuThr 2074
Db 6339 CCTAGGGACACCTCGATCCTGCAGAGCCCTGGTGAGAAAACCCCGGTGAGCGCGGTGACC 6398
QY 2075 ArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGln 2094
Db 6399 CAG-----GGGGGCTCCCTGCAGTCCCCACCACCGTCCCCACGGGCC 6440
QY 2095 SerLysVal-----SerLysHis-----IleArgLeuProAlaPro 2106
Db 6441 GCCAGCGTCGCGCACTCGTAAGCATACCTTCGGACAGCACTGCGTCTCCAGCGCGCGCGG 6500
QY 2107 CysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGlu 2126
Db 6501 GCCCCAGCGGAGAGGAGCGCGAGCCCTCGGACCCA----- 6536
QY 2127 LeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro---SerSerGlnGluGlu 2145
Db 6537 GCCGACGAGAGGTTCAGCCACATCACCAGCTCCGCTGCCCCCTGGCAGCCACAGCCGAG 6596
QY 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyr 2156
Db 6597 CCCCATGGCCCCGAAGCCTCTCCGGTGGCGCGGCGGAGCGGACCTGGCAGGCTCTAC 6656
QY 2157 SerValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArg 2176
Db 6657 AGCGTGGACGCTCAGGGCTTCTTGACAAGCCGGGC---CGGGCAGACGAGCAGTGGCGG 6713
QY 2177 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerPro 2196
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Db 6714 CCCTCGCGGGAG-----CTGGGCAGCGGGGAG-----CCTGGGGAG 6749
QY 2197 SerSerLeuGlyGlyGlnProLeuGlyGlyPro-----GlySerArgProLysLysLys 2214
Db 6750 GCGAAGGCCTGGGGC---CCTGAGCGCGAGCCCGCTCTGGGTGCGCGCAGAAAGAAG 6806
QY 2215 LeuSerProProSerIleSerIleAspProPro---GluSerGlnGlySer---ArgPro 2232
Db 6807 ATGAGCCCCCTGTCATCTCGGTGGAACCCCTGCGGAGGACGAGGGCTCTGCGCGGCC 6866
QY 2233 ProCysSerProGly-----ValCysLeuArgArgAlaProAlaSerAspSerLys 2250
Db 6867 TCCGCGGCAGAGGGCGGCGCAGCACACACTGAGGCGCAGGACCCCGTCTCTGTGAGGCCACG 6926
QY 2251 AspProSerValSer---SerProLeuAspSerThrAlaAlaSerProSerPro----- 2267
Db 6927 CCTCACAGGAATCCCTGGAGCCACACAGAGGGCTCAGGCGCCGCGGGGGACCTGCAGCC 6986
QY 2268 -----LysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6987 AAGGGGAGCGCTGGGGCCAGGCCTCTCTGCCGGGTGAGCACCTGACCGTCCCCAGCTTT 7046
QY 2278 SerSerAspProThrAspMet-----AspPro 2286
Db 7047 GCCTTTGAGCCGCTGGACCTCGGGGTCCCCAGTGGAGACCCT 7088

RESULT 5
US-09-398-522-51
; Sequence 51, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
; NAME/KEY: CDS
; LOCATION: (373)... (3993)
US-09-398-522-51

Alignment Scores:
Pred. No.: 0 Length: 3993
Score: 6103.00 Matches: 1173
Percent Similarity: 95.49% Conservative: 12
Best Local Similarity: 94.52% Mismatches: 52
Query Match: 50.74% Indels: 4
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-398-522-51 (1-3993)

QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 281 CCGCGGGGGCCCCCGGGTTGCGTGAGGACACCTCTCTGAGGGGCGCGCTTGCCCTCT 340
QY 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGGCCCCCGCTGGCCAGAGGATGACGAGGAGGAGGATGAGCGGGCG 400
QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
Db 401 CCGAGGAGTGGGACAGCCCCCGGAGCTTCATGCGGCTCAACGACCTGTTCGGGGCGGGG 460
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QY	63	Ala-AlaGlyVala-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG	82
Db	461	GCCGGCCGGGGCCGGGTCAGCAGAAAAGACCCGGCAGCGCGACTCCGAGCGGAGG	520
QY	82	lyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgp	102
Db	521	GGCTGCCGTACCCGGCGCTGGCCCGGTGGTTTCTTCTACTTGAGCAGACAGCCGCC	580
QY	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	122
Db	581	CGCGGAGCTGGTGTCTCCGACGGTCTGTAAACCCCTGGTTTGAGCGCATCGATGTTGG	640
QY	122	alileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142
Db	641	TCATCCTTCTCAACTGCGTGACCCCTGGGCATGTTCGGCCATCGCAGACATCGCCTGTG	700
QY	142	spSerGlnArgCysArgileLeuGlnAlaPheAspPheilePheAlaPhePheAlav	162
Db	701	ACTCCAGCGCTGCCGATCCTGCAGGCCCTTGATGACTTCATCTTTGGCTTCTTTGCCG	760
QY	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA	182
Db	761	TGGAGATGGTGGTAAGATGGTGGCCTTGGGCATCTTTGGGAAAAGTGTACCTGGGAG	820
QY	182	spThrTrpAsnArgLeuAspPhePheileValileAlaGlyMetLeuGluTyrSerLeuA	202
Db	821	ACACTTGGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGGATGCTGGAGTACTCGCTGG	880
QY	202	spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
Db	881	ACCTGCAGAACGTCAGCTTCTCAGCTGTCAAGACAGTCCGTGTGTGCGACCGCTCAGGG	940
QY	222	laileAsnArgValProSerMetArgileLeuValThrLeuLeuLeuAspThrLeuProM	242
Db	941	CCATTAAACCGGTGCCAGCATGCGCATCCTTGTACGTTGCTGTGGATACGCTGCCCA	1000
QY	242	etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheilePheGlyIleValGlyV	262
Db	1001	TGCTGGGCAACGTCCTGCTGCTCTGCTTCTTCGTCTCTTCTTCATCTTCGGCATCGT	1060
QY	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeup	282
Db	1061	TCCAGCTGTGGCAGGGTGCTTCGGAACCGATGCTTCTACCTGAGAAATTCAGCCTCC	1120
QY	282	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI	302
Db	1121	CCCTGAGCGTGGACCTGGAGCGCTATTACCAGACAGAGAACGAGATGAGAGCCCTTCA	1180
QY	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	1181	TCTGTCTCCAGCCACCGCAGAACGGCATGCGGTCTTCGAGAAGCGTGCCACGCTGCGCG	1240
QY	322	lyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerA	342
Db	1241	GGGACGGGGCGGTGGCCACCTTGGGTCTGGACTATGAGGCCTACAACAGCTCCAGCA	1300
QY	342	snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP	362
Db	1301	ACACCACCTGTGTCAACTGGAACCCAGTACTACACCACTGCTCAGCGGGGAGCACAACC	1360
QY	362	roPheLysGlyAlaileAsnPheAspAsnileGlyTyrAlaTrpIleAlailePheGlnV	382
Db	1361	CCITTCAAGGGCGCCATCAACITTGACAAACATTGGCTATGCTGGATCGCCATCTTCCAGG	1420
QY	382	alileThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	1421	TCATCAGCTGGAGGGCTGGGTGACATCATGTACTTTGTGATGGATGCTCATTCCTCTCT	1480
QY	402	yrAsnPheileTyrPheileLeuLeuileileValGlySerPhePheMetIleAsnLeuC	422
Db	1481	ACAAATTTCATCTACTTTCATCCTCATCATCGTGGGCTCCTTCTTCATGATCAACCTGT	1540
QY	422	ysLeuValValileAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMeta	442

Db	1541	GCCTGGTGGTGATTGCCACGCAGTTCTCAGAGACCAGCAGCGGGAAGCCAGCTGATGC	1600
QY	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1601	GGGAGCAGCGTGTGCGGTTCTGTCCAACGCCAGCACCCCTGGCTAGCTTCTCTGAGCCCG	1660
QY	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
Db	1661	GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGATCATCTTCGTAAAGCAGCCCGCA	1720
QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1721	GGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGCGGTTGGGCTGCTCAGCAGCCAGCAC	1780
QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1781	CCCTCGGGGGCCAGGAGACCCAGCCAGCAGCAGCTGCTCTCGCTCCCACCGCCGCTAT	1840
QY	522	erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisLeuGlyAsnG	542
Db	1841	CCGTCCACCACCTGGTGACCCACCACCACCATCACCACTACCACTACCACTGGGCAATG	1900
QY	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGGATGCCAATGGTCCC	1960
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGGCTCATGTGCCACCACCCTCGACGGCTGCCCTCTCCGGGGCCCCCTGGTGGCG	2020
QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGCACAGCTTCTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2080
QY	602	laProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCCATCTGAGGCATCCGGCAGGACTGTGGCAGCGGGAAGGTGT	2140
QY	622	yrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCACCGTGCACACCAGCCCTCCACCGGAGACGCTGAAGGAGAGAGGCACTAGTAGAGG	2200
QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2201	TGGCTGCCAGCTCTGGGCCCCAACCTTCACAGCCTCAACATCCCACCCGGGCCCTACA	2260
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGCACAAGCTGTGGAGACACAGAGTACAGGTGCCTGCCAAAGCTTTGCAAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCCAGCCCTTGCTTGAAGCAGACAGTGGAGCCTGTGGTCCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2381	GTGCCCCGGGGCAGGGAGGTGGAGCTCGCCGACCGTGAAATGCCTGACTCAGACA	2440
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2441	GCGAGGCAGTTTATGAGTTCACACAGGATGCCAGCACAGCGACCTCCGGGACCCCCACA	2500
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC---CGGGGGCAACGGAGCCTGGGCCCCAGATGCAGAGCCAGCTCTGTGCTGGCTTCT	2557
QY	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2558	GGAGGCTAATCTGTGACACCTTCGAAAAGATTGTGGACAGCAAGTACTTTTGGCCGGGAA	2617
QY	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802

Db 2618 TCATGATCGCCATCCTGGTCAACACACTCAGCATGGGCATCGAATACCACGAGCAGCCG 2677

Qy 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822

Db 2678 AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTACCAGCCTCTTTGCCCTGG 2737

Qy 822 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842

Db 2738 AGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTTGGCTACATCAAGAATCCCTACAACA 2797

Qy 842 lePheAspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyGlyG 862

Db 2798 TCCTTCGATGGTGTCAATTGTGGTTCATCAGCGTGTGGGAGATCGTGGGCCAGAGGGGGCG 2857

Qy 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882

Db 2858 GCCTGTGGTGTGTCGGACCTTCGCGCTGATGCGTGTGCTGAAGCTGGTGCCTTCCTGC 2917

Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902

Db 2918 CGCGCTGCAGCGGCAGCTGGTGTCTCATGAAGACCATGGACACGTGGCACCTTCT 2977

Qy 902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922

Db 2978 GCATGCTGCTTATGCTCTTCATCTTCATCTTCAGCATCCTGGGCATGTCATCTTCGGCT 3037

Qy 922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942

Db 3038 GCAAGTTTGCCTCTGAGCGGGATGGGGACACCCCTGCCAGACCGGAAGAAATTTGACTCCT 3097

Qy 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962

Db 3098 TGCTTGGGCCCATCGTCACTGTCTTTCAGATCCTGACCAGGAGGACTGGAAACAAAGTCC 3157

Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982

Db 3158 TCTACAATGGTATGGCCTCCACGTCTCCTGGCGGCCCTTATTTTCATTGCCCTCATGA 3217

Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002

Db 3218 CCTTCGGCAACTACGTGCTCTTCAATTGCTGGTCGCCATTCTGGTGAGGGCTTCCAGG 3277

Qy 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022

Db 3278 CGGAGGGAGATGCCAACAAAGTCCGAATCAGAGCCCCGATTCTTCTCACCCAGCCTGGATG 3337

Qy 1022 lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042

Db 3338 GTGATGGGGACAGGAAGAGTGCTTGGCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGC 3397

Qy 1042 rgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062

Db 3398 GGAAGAGCCTGTGCCGCTCTCATCCACACGCGCGCCACACCCCATGTCGCTGCCCA 3457

Qy 1062 ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers 1082

Db 3458 AGAGCACCGACAGCGGCTGGCGAGGCGCTGGGCCCTGCGTCGCGCGCACCGACGACA 3517

Qy 1082 erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102

Db 3518 GCGGGTGGCAGAGCCTGGGGCGGCC--CACGAGATGAAGTCACCGCCCCAGCGCCGCA 3574

Qy 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA 1122

Db 3575 GCTCTCCGCACAGCCCCCTGGAGCGCTGCAAGCAGCTGGACCAGCAGCGGCTCCAGCCGGA 3634

Qy 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142

Db 3635 ACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGAGAGCCCAAGTGGAGAGCGCGGTCCC 3694

Qy 1142 euLeuSerGlyGluGlnGlnSerGlnAspGluGluSerSerGluGluAspArgA 1162

Db 3695 TGTGTGCGGAGAGAGGCCAGGAGAGCCAGGATGAAGAGGAGAGCTCAGAAAGAGGAGCGGG 3754

Qy 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS 1182

Db 3755 CCAGCCCTGCGGGCAGTGACCATGCCACAGGGGGTCCCTGGAGCGGGAGGCCAAGAGTT 3814

Qy 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202

Db 3815 CCITTGACCTGCCAGACACACTGCAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG 3874

Qy 1202 erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222

Db 3875 GGTCGTCTTGAGCACCAAGGACTGCAATGGCAAGTCGGCTTCAGGGCGCCTGGCCCGGG 3934

Qy 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsnLeu 1241

Db 3935 CCCTGCGGCCTGATGACCCCCCACTGGATGGGGATGACGCCGATGACGAGGGCAACCTG 3993

RESULT 6

US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-1 (1-6816)

Qy 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCCCTCCTCATCTGCAGCAGCCCGCTGAGCCAGGAGTCAACCGAGCAG 266

Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCCGGACCCCGG----- 278

Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCAGGCTGGAGGAGCCTCTGGATGGAGCT----- 326

Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344

Qy 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCCTATTGCCTTCTTCTGCCTGCACAGACCACCGCCCCCGAACTGG 404

Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGTGGTTTGAATGTGTGAGCATGTGTGTGATCCTGCTG 464

QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
 Db AACTGCGTGACACTTGGCATGTACCAGCCGTGCGACGACATGGACTGCCTGTCCGACCGC 524
 QY 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
 Db TGCAAGATCCTGCAGGTCTTGTATGACTTCACTTCTTATCTTCTTGGCATGGAGATGGTG 584
 QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTyrAsn 185
 Db CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAGTGCTACCTCGGGACACATGGGAAC 644
 QY 186 ArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
 Db CGCCTGGATTCTTCATCGTCATGGCAGGGATGGTCGAGTACTCCTCTGGACCTTCAGAAC 704
 QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
 Db ATCAACCTGTACGCCATCCGCACCGTGGCGTCTGAGGCCCTCAAGCCATCAACCCGC 764
 QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
 Db GTGCCCCAGTATCGGATTCCTGGTGAACCTGCTCTGGACACACTGCCCATGCTGGGGAAT 824
 QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
 Db GTCTGTCTGCTCTGCTTCTTGTCTTCTTCTTCTTGGCATCATAGGTGTGCAGCTCTGG 884
 QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
 Db GCGGCCCTGCTGCGTAACCGCTGCTTCTTGGAGGAGAACTTCAACCATACAAGGGATGTG 944
 QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
 Db GCCTTGCCCCCATACTACCGCCGAGGAGGATGATGAGATGCCCTTCATCTGCTCCCTG 1004
 QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
 Db TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
 QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
 Db 1059 ---GGCCGTGAGTGTGCTGTCCAAGGACGAGCTTACGACTTTGGGGCGGGCGCCAG 1115
 QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
 Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGTTACTACAATGTGTGCCGCACG 1175
 QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
 Db 1176 GGCAGCGCCAACCCCCACAAGGTGCCATCAACTTGAACAACATCGGTTATGCTTGGATT 1235
 QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
 Db 1236 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGAT 1295
 QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
 Db 1296 GCTCACTCTTCTACAACTTCATCTACTTTCATCTGCTTATCATAGTGGGCTCTTCTTC 1355
 QY 418 MetIleAsnLeuLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
 Db 1356 ATGATCAACCTGTGCTCGTTGTATAGCGACCCAGTCTTCGGAGACCAAGCAACGGGAG 1415
 QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
 Db 1416 CACCGGCTGATGCTGGAGCAGCGGCAGCGCTACCTGTCC---TCCAGCACGGTGGCCAGC 1472
 QY 458 PheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArg 477
 Db 1473 TACGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTCGC 1532

QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
 Db 1533 AAGGCCAAGCGC-----CGGCCCTGGGCTCTACAGGCCCTGCAG 1574
 QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
 Db 1575 AGC----- 1577
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QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
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Db 5687 CCCACCTGG-----CCGCAAGGACAGCAAGGTGAGCTGGACCCACCTGAGCCCAT 5737
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RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
DB: 4 Gaps: 60

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QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
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QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCCTATTGCCCTTCTTCTGCCTCGCAGACACCACAGCCCCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGTTTGAATGTGTGAGCATGTGTGATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
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QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
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Db 5471 GCCTGCCAGGACTCCTTGGAGGGGAGTGACCATCATCGAACACCTGTGGGCTCAT 5530
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
Db 5531 CTTCCACCACCTACTCCTCGCCTGCCGCTGCCGCTGCAAGAAAGTGCA-----CCA 5575
QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
Db 5576 CGACAA-----GCAAGAGGTGCAGCTGGCTGAGACGGA 5608
QY 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
Db 5609 GGCCTTCTCCTGAACCTCAGACAGGTCTCTGTCATCCTGCTGGTGACGACCTGAGTCT 5668
QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
Db 5669 CGAGGA-----CCCCACAGCCTG 5686
QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
Db 5687 CCCACCTGG-----CCGAAGGACAGCAAGGTGAGCTGGACCCACCTGAGCCCAT 5737
QY 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla 2045
Db 5738 GCGTGTGGGAGACCTGGGGAATGCTTCTTCCCTTGT-CCTCTACGCGCGTCTCGCCGG 5796
QY 2046 IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGlu 2065
Db 5797 ATCCAGAGAACTTCTCTGT--GTGAGATGGAGGATCCCAT-----TCAACC 5841
QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlySerIle 2085
Db 5842 CTGTCCGGTCTCGCTGAAACATGACA----- 5868
QY 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
Db 5869 -----GCAGTCAAGCACCCCAAGTCCCTTCT 5895
QY 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
Db 5896 CCC-----CGGATGCCTCCAGCC----- 5913
QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu 2145
Db 5914 -----CTCTCTGCCCATGCCAGCCGAGTCTTCCACCCTG 5949
QY 2146 ProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSerCys 2163
Db 5950 CAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGCACTGGCACTGGAAACCTCCCCAAGA 6009
QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
Db 6010 TTGCGCTG-CAGGGCTCTCTGGGCATCT-----CTGCGGTACCAAGGTCAACTGT 6059
QY 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCTCCGGCAGGCCACCGGAGCGACACGTCGCTGGACGCCAGCCCCAGCAG-CTC 6118
QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer 2219
Db 6119 CGCGGGACCTGCAGACCACGCTCGAGGACAGCCTGACCTGAGCGACAGCCCCCGGG 6178
QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGCCCTGGGGCGCCCGCCGCTGCTCCAGGACCCCGGC 6217
QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257

Db 6218 CGGCGCTGTCCCCCGCGCTCGCGCGCGCTGAGCCTGCGGGCGCTCTTACGCCT 6277
QY 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGCGGGCGCATCAGCGCAGCCACAGCAGCGGGGCTCCACCAGCCCGGGCTG 6337
RESULT 8
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3
Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 3 Gaps: 63
US-09-611-257A-24 (1-2287) x US-09-404-650-3 (1-6855)
QY 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCCTCCTCATCTGCAGAGCCCGCAGCGCTGAGCCAGGAGTCAACCAGGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCCCGCAGGCTGGAGGAGCCTCTGGATGGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCCTATTGCCTTCTTCTGCTGCGACAGACCACCGCCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGTGGTTGAATGTGTACAGCATGTGTGGTATCTCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCAGCCGTGCGACGACATGGACTGCCTGTCCGACCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGCAAGATCCTGCAGGTCTTTGATGACTTCACTTATCTTCTTTGCCATGGAGATGGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185

Db 585 CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAAGTGCTACCTCGGGACACATGGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGGATTCTTCATCGTTCATGCGAGGGATGGTCGAGTACTCCCTGGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTAGCCATCCGCACCGTGGCGCTCCTGAGGCCCTCAAAGCCATCAACCCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGCGGATCCTGGTGAACCTGCTCCTGGACACACTGCCCATGCTGGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCCTGCTGCTGCTGCTTCTTGTCTTCTTCATCTTTGGCATCATAGGTGTGCAGCTCTGG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGGCCTGTGCGTAACCGCTGCTTCCTGGAGGAACTTCACCATACAAGGGGATGTG 944
QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPropheIleCysSerGln 305
Db 945 GCCTTGCCCCATACTACCAGCCGAGGAGGATGATGAGATGCCCTTCATCTGCTCCCTG 1004
QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGGCGACAATGGGATATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 --GGCGTGAGTGCTGCCTGTCCAAGGACGACGCTCTACGACTTTGGGGCGGGGCCAG 1115
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGCAG 1175
QY 358 GlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCAAACCCCAAGGGTGCCATCAACTTTGACAAATCGGTTATGCTTGGATT 1235
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGAT 1295
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCCTTCTACAACCTTCATCTACTTTCATCCTGCTTATCATAGTGGGCTCTCTTC 1355
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCCTCGTTGTATAGCGACCCAGTTCTCGGAGACCAAGCAACGGGAG 1415
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGGAGCAGCGGCGGCTACCTGTCC---TCCAGCACGGTGGCCAGC 1472
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGCTGCCACATCTCGCG 1532
QY 478 LysAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCCCTTACCAGGCCCTGCAG 1574
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyr 537
||||| : : : :

Db 1578 ---CGCGCCAGGCCCTG----- 1592
QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
QY 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGGCCCGCCCAACCTGGGCC----- 1628
QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CAGCCCAAG-----GAGCCC 1643
QY 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCACTGTGCCCGCAACATAGCCCCCTGGATCG----- 1685
QY 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGCTGAG-----CCCATCCCCCGCCACGCTGGCTTC----- 1730
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCGCCAGCTGCCCTTGTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGACGGCCGGCGGCTCGGGCCTGGGCAGCACCGACTCGGGCCAGGAGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCAGGACGAGGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACCGGGCC-----CGGAGCAGCAGGAGCAGGAGCCTCTCCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGAAGGAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGCG 1940
QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCGTGCTGTGGGGATGTGTGGCGGGAGAGCGCGAGCCAAAGCTGCGCGGCATCGTGGAC 2000
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGATCATGATGGCCATCCTGGTCAACACCGTCAGCATGGGC 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCGAGCACCAAGCAGCAGCGGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGGTC 2120
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPropheGly 834
Db 2121 TTCACCAGCATGTTTCCCTTGAGATGATCTCCTGAAGCTGGCTGCATTTGGGCTCTTCGAC 2180
QY 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGlu 854
Db 2181 TACCTGGCTAACCCCTACAACTCTTCGACAGCATCATTTGTTCATCATCAGCATCTGGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGGCAGGGCGGACGGTGGGCTGTCCGTGCTGCGGACCTTCCGGCTGCTGCGCGTG 2300
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGGTGGCTTCATGCTGCCCTGCCCTGCGGCGCAGCAGTCTCGTGTGCTCATGAAGACC 2360

QY	1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
Db	3390	GCCAAAGACGTCTTACCAAGATGGCGGACCGCGGGATCGCGGGAGGATGAGGAGGAA	3449
QY	1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Db	3450	ATCGACTACACCCCTGTGCTTCCGCGTCCGCAAGATGATCGACGCTCTATAAGCCCGACTGG	3509
QY	1259	CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeu	1278
Db	3510	TGCGAGGTCCGCGAAGACTGGTCTGTCTACTCTTCTCTCCCGAGAACAGGTTCCGGGTC	3569
QY	1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298
Db	3570	CTGTGTCTCAGACCATATTATGCCCCAACAACTCTTCGACTACGTCTCTTGGCCTTCATCTTT	3629
QY	1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
Db	3630	CTCAACTGCATCACCATCGCCCTGGAGCGGCCTCAGATCGAGCCGCGCAGCACCGAACGC	3689
QY	1319	IlePheIleuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
Db	3690	ATCTTTCTCACCGTGTCCAACTACATCTTTCACGGCCATCTTCGTGGCGAGATGACATTG	3749
QY	1339	LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358
Db	3750	AAGGTAGTCTCGTGGCCCTGTACTTCGGCGAGCAGCGGTACCTACGCAGCAGCTGGAAC	3809
QY	1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
Db	3810	GTGCTGGATGGCTTTCTTGTCTTGTGTCTCATCATCGACATCGTGGTGTCCCTGGCCTCA	3869
QY	1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db	3870	GCCGGGGAGCCAAAGATCTTGGGGTCTCTCGAGTCTTGGGCTCCTTGGCACCCTACGC	3929
QY	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
Db	3930	CCCCCTGCTGTATCATCAGCCGGGCGCGGGCTTGAAGCTGGTGGAGACACTCATCTCC	3989
QY	1419	SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly	1438
Db	3990	TCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGTGTGCTTCTTTCATCATCTTTGGC	4049
QY	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
Db	4050	ATCCTGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCACCTGTCTGGCGTGGACACCGCG	4109
QY	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
Db	4110	AACATCACCAACCGCTCGGACTGCATGGCGCCCAACTACCGCTGGTCCATCACAAATAC	4169
QY	1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db	4170	AACCTCGACAACCTGGGCGAGGCTCTGATGTCCCTCTTTGTCTGGCATCCAAGGATGGT	4229
QY	1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
Db	4230	TGGGTGAACATCATGTACAATGGACTGGATGGTGTGTGTGGACCAGCCTGTGACC	4289
QY	1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db	4290	AACCAACACCCCTGGATGCTGTACTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4349
QY	1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db	4350	GTGCTCAACATGTTTGTGGTGTCTGGTGGAGAACTTCCACAAGTGGCGGACGACCCAG	4409
QY	1559	GluGluGluAlaAlaArgArgArgGluGluLysArgLeuArgArgLeuLysLysArg	1578
Db	4410	GAGGCTGAAGAGGCACGGCGCGGTGAGGAGAGCGGCTGCGGCGCTGGAGAAAGACGC	4469
QY	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598

QY	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle	914
Db	2361	ATGGACAACGTGGCCACCTTCTGCATGCTGTCTCATGCTCTTTCATCTTTCAGCATC	2420
QY	915	LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu	933
Db	2421	CTTGGGATGCATATTTTGGCTGCAAGTTTCAGCCTCCGACGACACTGGAGACAGGTG	2480
QY	934	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	953
Db	2481	CCGACAGGAAGAACTTCGACTCCCTGCTGTGGCCATCGTCACTGTGTTCAGATCCTC	2540
QY	954	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	973
Db	2541	ACCCAGGAGGACTGGAAACGTCGTTCTTACAAATGGCATGGCCTCCACTTCTCCCTGGGCG	2600
QY	974	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	993
Db	2601	TCCCTCTACTTTGTGCGCCCTCATGACCTTCGGCAACTATGTGCTTTCAACTGTGTGTG	2660
QY	994	AlaIleLeuValGluGlyPheGlnAlaGluGlyAlaThrLysSerGluSerGluPro	1013
Db	2661	GCCATCTGGTGGAGGCTTCCAGCGGAGGTGACGCCAATCGTCTCTACTCGGACGAG	2720
QY	1014	AspPhePheSerProSerVal-----AspGlyAsp	1023
Db	2721	GACCAGAGCTCATCCAACATAGAAAGATTGTATAAGCTCCAGGAAGGCTGGACAGCAGC	2780
QY	1024	GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys	1043
Db	2781	GGAGATCCCAAG-----CTCTGCCCAATCCCCATGACCCCAATGGGCACCTGGACCCC	2834
QY	1044	SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer	1059
Db	2835	AGTCTC-----CCACTGGTGGGCACCTAGGTCTCTGTGGGCTGCGGGACCTGCC---	2885
QY	1060	HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr	1079
Db	2886	---CCCCGACTCTCACTGCAGCGCGGACCCCATGCTGTGTGGCCCTGGGCTCCGAAAGAGC	2942
QY	1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer	1099
Db	2943	AGTGTATGTCTCTA-----GGGAGGATGAGCTATGACGAGCGCTCCCTGTCCAGC	2993
QY	1100	AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119
Db	2994	TCCCGGAGCTCCTACTACGGGCCATGGGCGCGCAGCGCGGCTGGGCCAGCCGTCGCTCC	3053
QY	1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg	1139
Db	3054	AGCTGGAAC-----ACCTCAAGCACACAAGCCGCGCTCGGCGGAGCAT	3095
QY	1140	ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu	1158
Db	3096	GAGTCCCTGCTCTCTGCGGAGCGCGGCGCGGCTGTGCGAGGTTGCCCGGAGC	3155
QY	1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3156	GAGGGCGCGCGCGGCGCGCACCCCTGCACACCCACAGCCCGGACCATTCATCAGGG	3215
QY	1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
Db	3216	CCCCATCTGGCGCACCGCCACCGCCACCGCGGACGCTGTCTCCTCGACAACAGGGAC	3275
QY	1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
Db	3276	TCGGTGGACCTGGCCGAGTGTGTCGCGGTCGCGGTCGCGGCCCCACCCCGGCGCGCTGGAGG	3335
QY	1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
Db	3336	CGGGCAGGCCCGGCCCCCGGGGATGAGGACTGCAATGGCAGGATGCCAGC-----ATC	3389

Db 4470 CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACCTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCCGGCTGCTCATCCACTCCATGTGCACCGCCACTACCTGGACATCTTCATCACC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db 4569 TTCATCATCTGCCTCAACGTGGTCAACCATGTCCCTGGAGCACTACAATCAGCCACGTCC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCAACCACTGTCTTTGTGTGGAGGCT 4688
QY 1659 ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrAsnGlnLeu 1678
Db 4689 GTGCTGAAGCTGGTGGCATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGTGCTACTGTCACTCATGGGCATCACCTCGGAGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 GCGGCCCTGCCCATCAATCCCAACCATCATCCGCATCATGAGGGTTCTGCGCATTGCCCGA 4868
QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTGCTGAAGCTGTTGAAGATGGCCACAGGAATCGGGCCCTGCTGGACACGGTGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAla 1758
Db 4929 GCTTTGCCCCAGGTGGCAACCTTGGCCCTCCTCTTCATGCTGCTCTTCTCATCTATGCT 4988
QY 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
Db 4989 GCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db 5049 ATGACCGGCATGCCACCTTCGAGAACTTCGGCATGGGCTTCCTCACACTTCTCCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln 1817
Db 5109 TCCACGGGTGACAACTGGAACGGGATCATGAAGGACACGCTGCGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
Db 5169 GAGCGCAGCTGCCTGAGCAGCCTGCAGTTTGTGTCGCGCTGTACTTCGTGAGCTTCGTG 5228
QY 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
Db 5229 CTCACCGCGCAGTTTCGTGCTCATCAACGTGGTGGTGGTGTGCTCATGAAGCACCTGGAC 5288
QY 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMet 1875
Db 5289 GACAGCAACAAGGAGGCGCAGGAGGACGCGAGATGGATGCCGAGCTCGAGCTGGAGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro--- 1893
Db 5349 GCCATGGCCTGGCCCTGGCCCGAGGCTGCCATACCGGCTCCCGGGCGCC---CCTGGC 5405
QY 1894 -----GlyValGluGlyValAsnSerThrAsp----- 1902
Db 5406 CGAGGGCGGAGGGCGGGCGGGGGCGGACACCGAGGGCGGCTTGTGCGGCGCTGC 5465
QY 1903 ---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla 1917
Db 5466 TACTCGCTGC-CCAGGAGAACTGTGGCTGGACAGCGCTCTCTTTAATCATCAAGGACTC 5524
QY 1918 AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal 1937
Db 1937

Db 5525 CTTGGAGGG---GGAGCTGACCAT-----CATCGACAAACCTGTTCGGGCTC 5566
QY 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
Db 5567 CATCTTCCACCACCTACTCCTCGCCTGCCGGCTGCCAAGAAGTGTC----- 5611
QY 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACGACAA-----GCAAGAGGTGCAGCTGGTGAGAC 5644
QY 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5645 GGAGGCTTCTCCCTGAACCTCAGACAGGTCTCTGCTCCATCCTGCTGGGTGACACCTGAG 5704
QY 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCGAGGA-----CCCCACAGC 5722
QY 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
Db 5723 CTGCCACCTGG-----CCGCAAGACAGCAAGGGTGAGTGGACCCACCTGAGCC 5773
QY 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATGCGTGTGGAGACCTGGCGAATGCTTCTTCCCTTGT-CCTCTACGGCGCTCTCGC 5832
QY 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064
Db 5833 CGGATCCAGAGAACTTCTCTGT---GTGAGATGGAGGAGATCCCAT-----TCA 5877
QY 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSer 2084
Db 5878 ACCTGTCCGGTCTCTGGCTGAAACATGACA----- 5907
QY 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db 5908 -----GCAGTCAAGCACCCCAAGTCCCT 5931
QY 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSer 2124
Db 5932 TCTCCC-----CGGATGCTCCAGCC----- 5952
QY 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db 5953 -----CTCTCTGCCCCATGCCAGCCGAGTCTTCCACC 5985
QY 2145 GluProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGCAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGCACCTGGCACCTGGAAACCTCCCCA 6045
QY 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2182
Db 6046 AGATTGCGCTG-CAGGGCTCTCTGGGCATCT-----CTGCGGTCAACAAGGGTCAAC 6095
QY 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198
Db 6096 TGTACCTCTCTCCGGCAGGCCACCGGAGCGACACAGCTCGCTGGACGCCAGCCACGAGCAG- 6154
QY 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218
Db 6155 CTCGCGGGCAGCCTGCAGACCAACCGCTCGAGGACAGACCTGACCTGAGCGACAGCCCCCG 6214
QY 2219 SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db 6215 GCG-----TGCCCTGGGGCGCCCGCCCTGCTCCAGGACCCCG 6253
QY 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
Db 6254 GGCGGCTGTCCCCCGCGCTCGCCCGCTGAGCCTGCGCGCGGGGCTCTTTCAG 6313
QY 2257 ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db 6314 CCTGCGGGGCTGCGGGCGCATCAGCGCAGCCACAGCAGCGGGGCTCCACAGCCCCGG 6373

QY 2277 Leu 2277
Db 6374 CTG 6376

RESULT 9
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 4 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCCGCCCTCCTCATCTGCAGCAGCCCCAGCGCTGAGCCAGGAGTCACCACGGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCCGCCAGCGCTGGAGGAGCCTCTGGATGGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCCTATTGCCTTCTTCTGCTGGACAGACCACCAGCCCCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGTTGTTGAATGTGTGAGCATGTGTGTGATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCAGCCGTGGACGACATGGACTGCCTGTCCGACCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGAAGATCCTGCAGGTCTTTGATGACTTTCATCTTTATCTTCTTTGGCATGGAGATGGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185

Db 585 CTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGTACTCGGGACACATGGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGGATTTCTTCATCGTATGGCAGGGATGGTCGAGTACTCCCTGGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTGAGCCATCCGCACCGTGGCGCTCCTGAGGCCCTCAAAGCCATCAACCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGCGGATCCTGGTGAACCTGCTCCTGGACACACTGCCCATGCTGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCCTGCTGCTGCTTCTTTGTCTTCTTCATCTTTGGCATCATAGGTGTGCAGCTCTGG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGGCCTGTGCGTAACCGCTGCTTCTGGAGGAGAACTTCACCATACAAAGGGATGTG 944
QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGGCCCCCATACTACCAGCCGGAGGAGATGATGAGATGCCCTTCATCTGCTCCCTG 1004
QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGGCGACAATGGGATAATGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCCGTGAGTGTGCTGTCCAAGACGACGTCTACGACTTTGGGGGGGGCCAG 1115
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGACG 1175
QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCAAACCCCAAGGGTGCCATCAACTTTGACAACATCGTTATGCTTGGATT 1235
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCCAGTGATCACTCTGGAAAGGCTGGTGAGATCATGTACTACGTGATGGAT 1295
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCACTCCTTACAACTTCATCTACTTCATCCTGCTTATCATAGTGGGCTCCTTCTTC 1355
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGCTGTGTGTCATAGCGACCCAGTTCTCGGAGACCAAGCAACGGAG 1415
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGGAGCAGCGGCGAGCGGTACCTGTCC---TCCAGCACGGTGGCCAGC 1472
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TAGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTGTGCCACATCCTTCGCG 1532
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCCCTTACCAGGCCCTGCAG 1574
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537

Db 1578 ---CGGCGCCAGGCCCTG----- 1592

Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557

Db 1593 -----GGCCCGGAG----- 1601

Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577

Db 1602 -----GCCCGGCCCCCGCAACCTGGGCC----- 1628

Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597

Db 1629 -----CAGCCCAAG-----GAGCCC 1643

Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617

Db 1644 CGGCACTACCACTGTGCCCGCAACATAGCCCCCTGGATGCG----- 1685

Qy 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637

Db 1686 -----ACGCCCCACACC----- 1697

Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657

Db 1698 ---CTGTGCAG-----CCCATCCCCCGCACCGCTGGCTTCC----- 1730

Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676

Db 1731 -----GATCCCGCCAGCTGCCCTTGCTGCCAG 1757

Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696

Db 1758 CATGAGGACGGCGCGGCCCTCGGCCCTGGGCAGCACCGACTCGGGCCAGGAGGCTCG 1817

Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716

Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCGAGGACGAGGCG----- 1853

Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736

Db 1854 -----GATGGGACGGGGCC-----CGGAGCAGCAGGAGCAGGAGCCTCCTCAGAA 1898

Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756

Db 1899 CTGGGAAGGAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG 1940

Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774

Db 1941 GTCTGGCTGTGCGGGATGTGTGGCGGGAGACGCGAGCCAAGCTGCGCGGCATCGTGGAC 2000

Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794

Db 2001 AGCAAGTACTTCAACCGGGGCATCATGATGGCCATCCTGGTCAACACCCTCAGCATGGGC 2060

Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814

Db 2061 ATCGAGCACCACGAGCAGCCGGAGGAGCTGACCAACATCCTGGAGATCTGCAATGTGTC 2120

Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPropheGly 834

Db 2121 TTCACCAGCATGTTTGCCCTGGAGATGATCCTGAAGTGGTGCTGTCATTTGGGCTCTTCGAC 2180

Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGlu 854

Db 2181 TACCTGCGTAACCCCTACAACTCTTCGACAGCATCATGTGTATCATCAGCATCTGGGAG 2240

Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuSerValLeuArgThrPheArgLeuMetArgVal 874

Db 2241 ATCGTGGGGCAGGGCAGCGGTGGGTGTTCGGTGTGCGGACCTTCCGGCTGTGCGCGTG 2300

Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894

Db 2301 CTGAAACTGGTGGCTTTCATGCTGCCCTGCGGCGCCAGCTCGTGTGCTCATGAAGACC 2360

Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914

Db 2361 ATGGACAACGTGGCCACCTTCTGCATGCTGTCTCATGCTTCTTTCATCTTCAGCATC 2420

Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933

Db 2421 CTTGGGATGCATATTTTGGCTGCAAGTTTCAGCCCTCCGACGGACACTGGAGACACGGTG 2480

Qy 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953

Db 2481 CCGACAGGAAGAACTTCGACTCCCTGTGTGGCCATCGTCACTGTGTTCAGATCCTC 2540

Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973

Db 2541 ACCCAGGAGGACTGGAACGCTGTTCTCTACAATGGCATGGCCTCCACTTCTCCCTGGGCC 2600

Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993

Db 2601 TCCTCTACTTTGTGCGCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTGTCTGTG 2660

Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013

Db 2661 GCCATCCTGTGTGGGGCTTCAGGCGGAGGGTGAGCGCAATCGCTCCTACTCGGACGAG 2720

Qy 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023

Db 2721 GACCAGAGCTCATCCACATAGAAGAGTTTGATAAGCTCCAGGAAGGCTGGACAGCAGC 2780

Qy 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043

Db 2781 GGAGATCCCAAG-----CTCTGCCCAATCCCCATGACCCCCCAATGGGACCTGGACCCC 2834

Qy 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059

Db 2835 AGTCTC-----CCACTGGGTGGGCACCTAGGTCTCTGTGGGCTCGGGGACTGCC--- 2885

Qy 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079

Db 2886 ---CCCCGACTCTCACTGCAGCCGGACCCCATGTGGTGGCCCTGGGCTCCGAAAGAGC 2942

Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099

Db 2943 AGTGTATGTCTCTA-----GGGAGGATGAGTATGACCAGCGCTCCTGTCTCCAGC 2993

Qy 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119

Db 2994 TCCCGGAGCTCCTACTACGGGCCCATGGGCGCGAGCGCGCTGGCCAGCGCTCGCTCC 3053

Qy 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139

Db 3054 AGCTGGAAC-----AGCCTCAGACACAAGCCCGCTCGGCGGAGCAT 3095

Qy 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158

Db 3096 GAGTCCCTGTCTCTCGGAGCGCGCGCGCGCGGGTCTCGAGGTTGCGCGGAC 3155

Qy 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169

Db 3156 GAGGGGCCCGCGCGCGCGCACCCCTGCACACCCACACACGCCACCATTCATCACGGG 3215

Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181

Db 3216 CCCCATCTGGCGCACCGCCACCGCCACCCCGCGGACGCTGTCCCTCGACACACAGGAC 3275

Qy 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201

Db 3276 TCGGTGGACCTGGCCGAGCTGGTGGCGGGTGGCGGCCACCCCCGGGGCCGCTGGAGG 3335

Qy 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219

Db 3336 GCGGAGGCCCGGCCCTTCATGCTGAGGACTGCAATGGCAGGATGCCCAGC-----ATC 3389

Db 5525 CTTGGAGGG---GGAGCTGACCAT-----CATCGACAACCTGTGGGGCTC 5566

Qy 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957

Db 5567 CATCTTCCACCACTACTCTCGCTCGCGGTGCAAGAGTGTC-----5611

Qy 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977

Db 5612 CCACGACAA-----GCAAGAGGTGCAGCTGGCTGAGAC 5644

Qy 1978 GlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997

Db 5645 GGAGGCCTTCTCCCTGAACTCAGACAGGTCTCTGTCCTATCTGCTGGGTGACGACCTGAG 5704

Qy 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017

Db 5705 TCTCGAGGA-----CCCCACAGC 5722

Qy 2018 AlaProThrTyrGlyAlaIleProLysLeuProPro-----2029

Db 5723 CTGCCCCACCTGG-----CCGCAAGACAGCAAGGGTGAGCTGGACCCACCTGAGCC 5773

Qy 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044

Db 5774 CATGCGTGTGGGAGACCTGGGCGAATGCTTCTTCCCTTGT-CCTCTACGGCCGTCTCGC 5832

Qy 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064

Db 5833 CGGATCCAGAGAACTTCTCTGT---GTGAGATGGAGGAGATCCCAT-----TCA 5877

Qy 2065 GluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSer 2084

Db 5878 ACCCTGTCCGGTCTGGCTGAAACATGACA-----5907

Qy 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104

Db 5908 -----GCAGTCAAGCACCCCCCAAGTCCCT 5931

Qy 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSer 2124

Db 5932 TCTCCC-----CGGATGCTCCAGCC-----5952

Qy 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144

Db 5953 -----CTCTCTGCCCATGCCAGCCGAGTTCTTCCACC 5985

Qy 2145 GluProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSer 2162

Db 5986 CTGCAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGGCACTGGAACCCCTCCCCA 6045

Qy 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2182

Db 6046 AGATTGCGTGT-CAGGGCTCTGGGCATCT-----CTGCGGTCAACCAAGGTCAAC 6095

Qy 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198

Db 6096 TGTACCCCTCTCCGGCAGGCCACCGGAGCGACACGTCGCTGGAGCGCCAGCCCGCAGCAG- 6154

Qy 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218

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Qy 2219 SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro 2236

Db 6215 GCG-----TGCCCTGGGGCGCGCGCGCTGTCTCCAGACCCCG 6253

Qy 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256

Db 6254 GGCCGGCCTGTCCCCCGCGCTCGCGCCCGCTGAGCCTGCGCGGCGCGGCTCTTTCAG 6313

Qy 2257 ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly 2276

Db 6314 CCTGCGGGGGTGTGCGGCGCATCAGCGCAGCCACAGCAGCGGGGGTCTCCACCAGCCCGG 6373

Qy 2277 Leu 2277

Db 6374 CTG 6376

RESULT 10

US-09-404-650-12

; Sequence 12, Application US/09404650

; Patent No. 6309858

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/404,650

; CURRENT FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 6503

; TYPE: DNA

; ORGANISM: Rattus sp.

US-09-404-650-12

Alignment Scores:

Pred. No.: 0 Length: 6503

Score: 5407.00 Matches: 1234

Percent Similarity: 61.05% Conservative: 241

Best Local Similarity: 51.08% Mismatches: 502

Query Match: 44.95% Indels: 444

DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-12 (1-6503)

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Db 64 CCCCCGGGCGCGCCCTGCGCGGTCCCTCCCTCGCCCCGGGGCGCA-----114

Qy 23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTrpThrArgArgArg 38

Db 115 GCTGATCCCGGAATCCGAGCGGTGGGCGCGGGG-CGCGGGGTCCCTCTCCAGCGCGG 173

Qy 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla-----51

Db 174 CTTGGGGACACGCGTCACCCCGCGTCTCTGCGCGGACGACCCCGCTGCCCGCCACG 233

Qy 52 -----SerArgSerSerThrTh 57

Db 234 TCCATGCCAAGGGTCCCTGCTCCACGCTGACATGGGTGACAGCAACTTACCGCCCTCAT 293

Qy 57 rCysProGlyProGly-----AlaAlaGlyAla-GlySerThrG 70

Db 294 CTGCAGCAGCCCCCGCCCTGAGCCGGGAATCACTGAGCAGCCGGGCCCCCGGAGTCCCC 353

Qy 70 LuLysAspProGlySerAlaAspSerGluAlaGluGly-----LeuProTyrP 86

Db 354 CTCGATCCCTCCAGGCCCTGGAGGAGCCATTGGGAAGAAACCAACCTGACGTCACATC 413

Qy 86 roAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpC 106

Db 414 CAGACCTGGCTCCTGTTGCTTCTTCTGCTGCGGACAGCCACGAGCCCACTGGT 473

Qy 106 ysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuA 126

Db 474 GCATCAAGATGTTTGTAAACCGGTGGTTCGAGTGTGTGAGCATGCTGTTATTCTGCTGA 533

Qy 126 snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgC 146

Db 534 ACTGTGTGACCCCTGGGCATGTACCAGCCATGTGTGATGATGAGTGCCTGTGCGACCGTT 593

Qy 146 ysArgIleLeuGlnAlaPheAspAspPheIlePheAlaValGluMetValV 166

Db 594 GCAAGATCCTGCAGGCTTCGATGACTTTCATCTTCATCTTCTTTGGCATGGAGATGGTGC 653
QY 166 alLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsnA 186
Db 654 TTAAGATGGTGGCCCTGGGCATTTTGGCAAGAGTGCTACCTCGAGACACATGGAACC 713
QY 186 xgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnV 206
Db 714 GCCTGGATTTCTTCATTTGTCATGGCAGGGATGGTTGAGTACTCTCTGGACCTACAGAACA 773
QY 206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV 226
Db 774 TCAACCTGTAGCCATCCGACTGTGCGTGTCTGAGGCCTCTCAAAGCCATCAACCCGTG 833
QY 226 alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnV 246
Db 834 TACCCAGCATGCGGATCCTGGTGAACCTGTGCTCGACACGCTGCCATGCTGGGAACG 893
QY 246 alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266
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Db 1074 CTGGGGACAATGGCATATGGGCTGCCACGAGATCCCCCACCAGAGAGCAG----- 1126
QY 326 lyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSers 340
Db 1127 --GGCCGGGAATGCTGCCTGTCCAAAGATGATGTGTATGACTTCGGGGCGGGCGCCAGG 1184
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QY 930 ---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr 948
Db 2519 ACGGAGACACCGTTCCTGACAGGAAGAACTTCGATTCTTACTGTGGCCATCGTCACA 2578
QY 949 ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer 968
Db 2579 GTGTTCCAGATCCTCACTCAGGAGGACTGGAACGTTGTCTGTGTACAAATGGCATGGCCTCC 2638
QY 969 ThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu 988
Db 2639 ACCACCCCTGGCCTCCCTCTATTTTGTTGCCCTCATGACCTTTGGCAACTACGTTCTC 2698
QY 989 PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys 1008
Db 2699 TTCAATCTCCTGTTGGCTATCCTGTTAGAGGGTTTCCAGGCTGAGGGTGATGCTAATCGT 2758
QY 1009 SerGluSerGluProAspPhePheSerProSerProSerValAspGly----- 1022
Db 2759 TCCTGTCTGATGAGGACCAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCCAGAG 2818
QY 1023 -----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
Db 2819 GGCCTGGACAACAGTAGAGATCTCAAGCTCTGCCCAATACCCATGACACCCAATGGACAC 2878
QY 1041 LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet 1058
Db 2879 CTGGACCCCTAGCCTC-----CCTCTGGGTGCGCATCTGGGTCTGTGTACCATGGGT 2932
QY 1059 SerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 1078
Db 2933 ACTGCCCCCGCCTCTCACTGCAGCCAGACCCGGTACTGTGTGGCCTTAGACTCTCGGAAA 2992
QY 1079 ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProPro 1098
Db 2993 AGCAGTGTCTATCTCCCTG-----GGCAGGATGAGCTATGATCAGCGATCCTTGTCC 3043
QY 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg 1118
Db 3044 AGCTCCCGGAGCTCCTACTACGGGCCCTGGGGCCCGCAGTGGGACCTGGGCTAGCCGCCGC 3103
QY 1119 SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu 1138
Db 3104 TCCAGCTGGAAC-----AGCCTGAAACACAAGCCGCCCTCAGCTGAG 3145
QY 1139 ArgArgSerLeuLeuSerGlyGluGlnGluSer-----GlnAspGluGluGluSer 1156
Db 3146 CATGAGTCTTACTGTCTGGGAGGTGGAGGTAGTGTGCTCAGGGCCTGTGAAGGCGCC 3205
QY 1157 SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3206 CGGGAGGAGGGCGCAACTCGCACCCGACCCCTGTCATGTCTCCACACGCGCACCGCGCAC 3265
QY 1170 -----ArgHisArgGlySerLeuGluAla 1179
Db 3266 CATGGACCCACCTGGCACACCCGTCAACGACACCAACCCGCGGACTCTGTCCCTTGATACC 3325

Db 5405 ---GCCCATGGCCTCGGCCCTCGCCCTGGCCCTGCTGGT----- 5443

Qy 1914 HisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGlu 1933

Db 5444 -----CCCTGCCCTGC 5455

Qy 1934 GluValProValPro---LeuGlyProAspLeuLeuThrVal----- 1946

Db 5456 CCCTGCCCTCGCCCTGTGCTGGCCCGAGGCTGCCACTAGTTACCTGGGGTCCGGGG 5515

Qy 1947 ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn 1966

Db 5516 CGAGGATCGGAGGCGAGGTGCTGGAGGC---GACACCGAGAGTCACTGTGCCGGCAC 5572

Qy 1967 ---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGln 1985

Db 5573 TGTATTCTCCAGCCCGAGACCCCTG-----TGG-----CTGGAC 5608

Qy 1986 SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu 2005

Db 5609 AGCGTCTCTTAATCATCAAGGACTCCTTGGAGGGGAGCTGACCATCATTTGACAACCTG 5668

Qy 2006 ProLysAspVal---HisTyrLeuLeuGlnProHisGlyAla----- 2018

Db 5669 TCTGGTCCGTCTTCCACCACTAGCCCTCACTGACGGCTGTGGCAAGTGTCACCATGAC 5728

Qy 2019 -----ProThrTrpGlyAlaIleProLysLeuProProPro 2030

Db 5729 AAGCAAGAGACAGGTCTTCATCCATCTCTGCTGGGGATGACCTGAGTCTTGAGGACCCCA 5788

Qy 2031 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2050

Db 5789 CGGCCTGCCACAGGGCCCAAGGAGAGCAAGGTTGAAGTACTAGAGCCTCCGGAGCCCATGC 5848

Qy 2051 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu-----ValSerGly 2068

Db 5849 AGGCTGGAGACCTGGATGAATGCTTTTGGCCCTTGCCCAAGCGAGCGAGTGTCCACAGGC 5908

Qy 2069 ProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerIleGlnValGln 2088

Db 5909 CCAGAGAG-CCTGCTGTGGAGAT-----GGGGCCATTCCATTCAACC-CTG 5954

Qy 2089 GlnArgSerGlyIleGlnSerLysValSerLysHisIleArg----- 2102

Db 5955 TCCAGTCTGGCTCAACACGAGAGCAGCAAGCAAGCAGCCCTTCTCCCCGGGATG 6014

Qy 2103 -----LeuProAla 2105

Db 6015 GGTCCAGCCCTCTCTGTAGATGCCTGTGAGTCTTCCACCCCTGTGTGTCTGCCAGCC 6074

Qy 2106 -----ProCysProGly-----LeuGluPro 2112

Db 6075 AGAAGGGCAGGAACCGGGCATGAGTGCAGGAACCTGCCCAAG-ATTGCACTTCAGGGG 6133

Qy 2113 SerTrpAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu 2131

Db 6134 TCCTGGGCATCGCTGAGGTCAACCGAGTGTCAACTGCACCCCTCTTGGCCAGGCTACTGTG 6193

Qy 2132 SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAsp 2151

Db 6194 ACTGACACGTCCTTGGATGCCAGTCCCTAGCAGCTCA----- 6229

Qy 2152 LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeu 2171

Db 6229 -----SerAlaAspSerGluAla 80

Qy 2172 AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg 2191

Db 6230 -----GCGGGCAGCCCTACAGACCACACTGGAAGACAGTCTGACT----- 6268

Qy 2192 LeuCysProSerProSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro 2211

Db 6269 CTGAGTGACAGTCCCCCGGCTGCCCTGGGGCGCGGTCAGGTGCCCTGGG-----CCA 6322

Qy 2212 LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231

Db 6323 CGGGTAGCCTGTACCGGCCACCCCGCG-CCGCTCAGCCTGCGGGGCGGTGG 6376

Qy 2232 ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247

Db 6377 CCTGTTTAGTCTGCGTGGGCTGCGGGCCCATCAGCGTAGCCACAGCAGTGGCGGCTCCAC 6436

Qy 2248 -----AspSerLysAspProSer 2253

Db 6437 CAGCCCTGGCTGCACCTACCACGACTCCATGGACCCCTCT 6476

RESULT 12

US-09-949-016-15601

; Sequence 15601, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15601

; LENGTH: 70308

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-15601

Alignment Scores:

Pred. No.:	9.78e-114	Length:	70308
Score:	2055.00	Matches:	697
Percent Similarity:	21.05%	Conservative:	35
Best Local Similarity:	20.04%	Mismatches:	108
Query Match:	17.09%	Indels:	2640
DB:	4	Gaps:	21

US-09-611-257A-24 (1-2287) x US-09-949-016-15601 (1-70308)

Qy 4 HisArg-----ValProArg-----CysValArgThrProProLeuArgGly 17

Db 9479 CACAGGCATGATCGATTATTATCCCAATGGCTTGTGCAATAGTCAGGGTATTTGTGGC 9538

Qy 18 SerAlaArgProSerSerAspProProGlyProArgLeuAlaArg-----GlyTrpThr 35

Db 9539 TTGTCTTCTTTACAGATGAGGAAGCTGGGTCCAGAGAGGTGAGATGACCAAGGTGG--- 9595

Qy 36 ArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArgSer--- 54

Db 9596 -----GACTCCCTTCTCTGATGAGGAGTCTG 9622

Qy 55 -----SerThrThrCysProGlyAlaAlaGlyAlaGlySerThr 69

Db 9623 GGGCTGGGGCTGCTGCGTGTATGTACAGGGCCCTGGCACCCACACCTGCT---TAGCCT 9679

Qy 70 GluLysAspProGly-----SerAlaAspSerGluAla 80

Db 9680 CAGATGGAGCCAGGAGGTAAACGAGGAGGAGGTGTAGGGCGGGTCTGGGGCGGCCT 9739

Qy 81 GluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSer 100

Db 9740 CAGCTCCAGCCTGGCCAGCTGTTTCC----- 9766

Qy 101 ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet 120

Db	14121	TGCTCTGCTGAAGTTTTTAGCTCTCAGGACAAAGTCCTGTAGAGAGGGCATCCATCATAT	14180
QY	412	-----	412
Db	14181	AGTAGAGGGACACCAGATGCAGAGTCAGGAGGAAATCCAAGGTCAAGCGGACTTAAC	14240
QY	412	-----	412
Db	14241	TGCTATTGGGACCTTGGCAAGTCATTCTCCATGAGGCCCTCCAGCACTGCTCTGGGCGTC	14300
QY	412	-----	412
Db	14301	TGTTTCTCATGGGTAAATGAATGGTTCTCAACCTGAGATGATACCACCTCTCCAGAG	14360
QY	412	-----	412
Db	14361	GGCATTGGGAATGGAAAGGGTGATTCTGGTTTTTGATTTTTTTTAATAGCTTTATTGAG	14420
QY	412	-----	412
Db	14421	ACATAACTCACAATATCATTTCAATTCATCCCTTTGAATGAATCCAGTGGTTTTTTAAGCAT	14480
QY	412	-----	412
Db	14481	GTTTACAGAGTCTGTTTTTTTGTAAAGACAAGGGAGTGAATTTGGCAATTTGTACTG	14540
QY	412	-----	412
Db	14541	GGGAGGGGAGAGAAGCTAAACATCCTGAAATGCTTGCAATAAAGAATTAATCTACCCA	14600
QY	412	-----	412
Db	14601	AAATTCTGATCAGTGATCAATTGGTGTAAATGCTGCCTGATCTCTTATTCCTGCCAGTT	14660
QY	412	-----	412
Db	14661	CAGAAATTGCCAGACTTTAAGAAAGCAGAAAGACGGAGGCAAAAGCAGCAATATTAAATAG	14720
QY	412	-----	412
Db	14721	TTTTAATCACTACCATTATAGTTAATAACTTCAATCGCCACCACCTTTGAGCTAATATTA	14780
QY	412	-----	412
Db	14781	TTGAGCACTTACTATGCGCCAGCCCTGATCTAAGCACTTTCAATGTCTGTGCATTTA	14840
QY	412	-----	412
Db	14841	ATCCTCACCGTGATCCTCTCCATTTTACAGATGAGGAAACTGACATTTTCCTCATTTATCT	14900
QY	412	-----	412
Db	14901	GACCCTACCAGACGCTTTGCCTATGCTGTGTATTAATCTCCAAGAGTGGGGCATCACTGC	14960
QY	412	-----	412
Db	14961	TGACGTATGCTGTAAACATCTGCTGCCGTGTTAATCCTCGTCGTCCCTGTGAGGTGCCAG	15020
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Db	15021	GGCAGGATTTGGTCCCCATCTCTTAAATGAGAATTCAGCGCCCCAGAGGGTGGGTCAAC	15080
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Db	15081	TGGGCCAAGATCACACAGAAAGTAAGCGCTGGGGCTGAGAAATTCAGTCCCAGGCTAACG	15140
QY	412	-----	412
Db	15141	ACTCCACATTCAGCCCTTTCTTCCATGTCACCAAGAGGCCAACGACAGAGCCAGACAGAGG	15200
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Db	15201	GACAGACATTGAGAGAAAGAGATTAAAGAAAGATTAAGATCTACTCAGGACCTAGGACTAG	15260
QY	412	-----	412
Db	15261	CTCCAGAGAGAGATGAAGACAAATAAAGGCAGCTCCTTTGTGAGAGACAGAGGTAGGCC	15320
QY	412	-----	412
Db	15321	TGAGAAAGAGCAAGTCCCCAAGGCCACCTCATTTCTGCCTGCGTAACCTTCCCCTGGTGCGG	15380
QY	412	-----	412
Db	15381	AAGAGTGGCAGGCTTGGGGCGAAGCCTGACTGGAGGCCGTGTTCCCATCCCTGGGCCACCA	15440
QY	412	-----	412
Db	15441	CCTCAAGGGGTGAGGCCAGTGCTTCAGGGAAGTGGGGTCTTCTCACCATGTGCCCCCCCCC	15500
QY	412	-----	412
Db	15501	ACCCCCACTCCCTTTCCCTCCTGGGCTTGGGAGAGGGGAAGACAGACAGGGAGATA	15560
QY	412	-----	412
Db	15561	AGGGCCCTAGTTTCCACCCTCCACACACACCCCCCTGAAAAATCTTCTTAACAGCTCTCTG	15620
QY	412	-----	412
Db	15621	GAATCACACTAGTGAAGCTAATTATCATAATTACTAGGACACGATCTAGAAAAAATAAT	15680
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Db	15681	CTGCTTTGTCAACCATAAATATTCATTTCTTTCATTTGGGATGTTGTCCAAGCAATGGCT	15740
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Db	15741	GTTCCAGAGTTCTGGGAAACTGAGGCGTGAGATGGGGACTGGGGTAGTGTGAGCAAGT	15800
QY	412	-----	412
Db	15801	CAGGTGCGAGCCTGACTAGTCTGTAGGTCAGGGTTTCAGGGTTCCACACATCTCGAGGA	15860
QY	412	-----	412
Db	15861	GGGGGACAGGGAAAAATGGGGACAGACAAGGCCAATGGTCCCTGTTTTCAGATGAGGAT	15920
QY	412	-----	412
Db	15921	ATGAGGTCCCATGGCTAAGGTCTCTCGCCCCAAAGTCACACAGCTAGAAATGGGGCTAGA	15980
QY	412	-----	412
Db	15981	AGCAGGAGTCTGTAAATGATGTTTTTGTCAAGATCTCAAGGCTCAATATAATTTGAAAA	16040
QY	412	-----	412
Db	16041	CCCCATGTCCTTAATATTGCGTTTCATTTCCACAGCATTCGCTACTCCTAATGGAATTCG	16100
QY	412	-----	412
Db	16101	GGAAGGGGTGCTGCGTCTCTGCAGGTGTGCGTGTTTTAGGACAGGGAATTTGAGAGATTG	16160
QY	412	-----	412
Db	16161	CAGGATAACACCATGTTCAATAGCAATATCTTGGAATTTCAATAGAGCTTGGTTCAGTCT	16220
QY	412	-----	412
Db	16221	TAGCCTTGCTCTGAATTAGCTGAGTGATCTTGGGCAAAATGTTGACCTCTGTGGACCTGA	16280
QY	412	-----	412
Db	16281	GTTTCTTACCTGTCTGTATGGAGATTACAATAGCATCACCTCCTGAGGCTGTCTTAAAAA	16340

Db	2	TGCGGCTCCGAGCGCTGCAACATCCTTGGAGGCCCTTTGACGCGCTTCATTTTTCGCGCTTTT	61
QY	161	AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu	180
Db	62	GCGGTGGAGATGGTTCATCAAGATGGTGGCCTTGGGGTGTTGGGCGAAGATGTTACCTG	121
QY	181	GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer	200
Db	122	GGTGACACGTGGAACAGGCTGGATTTCTTCATCGTCTGGCGGGCATGATGGAGTACTCG	181
QY	201	LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuLeuAspThrLeu	220
Db	182	TTGGACGGACACAACGTAGCCTCTCGGCTATCAGGACCGTGGGTGCTGCGGCCCTC	241
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu	240
Db	242	CGCGCCATCAACCGCTGCCTAGCATGCGATCCTGGTCACTCTGCTGTGATACGCTG	301
QY	241	ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal	260
Db	302	CCCATGCTCGGAAACGTCCTTCTGCTGTGCTTCTTCGTCCTTCTTCATTTTCGGCATCGTT	361
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
Db	362	GGCGTCCAGCTCTGGGCTGGCCTCCTGCGGAACCGTGTCTCTCTGGACAGTGCCTTGTC	421
QY	281	LeuProLeuSerValAsp---LeuGluProTyrTyrGlnThrGluAsnGluAspGluSer	299
Db	422	AGGAACAACAACCTGACCTTCTGCGGCCGTACTACGACGGAGGGGGCGAGAGAAC	481
QY	300	ProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThr	319
Db	482	CCGTTTCATCTGCTCCTCAGCCGAGACAACGGCATGCAGAAAGTGTCTGACATCCCC	538
QY	320	LeuArgGlyGluGlyGlyGlyGlyProProCysSexLeuAspTyrGluThrTyrAsn---	338
Db	539	-----GGCCGCGGAGCTGCGCATGCCCTGCACCTGGCTGGGAGGCTACACGCAG	592
QY	339	-----SerSerSerAsnThrThrCysValAsnTrpAsnTrpAsnGlnTyrTyr	352
Db	593	CCGACGGCCGAGGGGTGGCGCTGCACGCAACGCCCTGCATCAACTGGAACCGTACTAC	652
QY	353	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	372
Db	653	AACGTGTGCGGCTCGGTGACTCCAAACCCCAACACGGTGCCATCAACTTCGACAAATC	712
QY	373	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAspIleMet	392
Db	713	GGCTACGCCTGGATTGCCATCTTCCAGGTGATCACGCTGGAAGGCTGGGTGGACATCATG	772
QY	393	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	412
Db	773	TACTACGTATGGACGCCACTCATTTCTACAACTTCATCTATTTCATCTGCTCATCATC	832
QY	413	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	432
Db	833	GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGGTATGCCACGCGAGTTCTCGGAG	892
QY	433	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	452
Db	893	ACGAAGCAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGGGCACGCCACCTGTCCAACGAC	952
QY	453	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	472
Db	953	AGCAGCTGGCCAGCTTCTCCGAGCCTGGCAGCTGCTACGAAGAGCTG-----	1000
QY	473	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal	492
Db	1000	-----	1000
QY	493	ArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGly	512
Db	1000	-----	1000

[illegible]

Db	707	GC GA	-----ACACTGAGGGCTGTGCGTGTGCTGAGGCCCTTGAAGCTGGT	751
Qy	223	eAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLe	243	
Db	752	GTCTGGGATTCCAAGTTGTCAGGTGGTCTCAAGTCCATCATGAAGCCCATGGTTC	811	
Qy	243	uGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValG1	263	
Db	812	CCTGCAGATTGGGCTGCTTCTCTCTTTGCCATCCTCATGTTGCCATCATTTGGCCTGGA	871	
Qy	263	nLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLe	283	
Db	872	GTTCTACATGGGCAAGTCCACAAGGCTGTTTC-----CCCAA	910	
Qy	283	uSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy	303	
Db	911	CAGCACAGATGCGGAGCCCGTG-----	932	
Qy	303	sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyG1	323	
Db	932	-----	932	
Qy	323	uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsnTh	343	
Db	933	-----GGTGACTCCCTGTGGCAAGGAGGCCCGCCGCGGTGTGCGAGGGCGACAC	985	
Qy	343	rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPh	363	
Db	986	TGAGTGC-----CGGGAGTACTGGCCA-----GGACCCAA	1015	
Qy	363	eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValI1	383	
Db	1016	CTTTGGGCATCACCAACTTGGACTGACATCCTCTATAATAACAAACGATGCGCGGCAACACCTG	1075	
Qy	383	eThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPheTy	402	
Db	1076	CACCATGGAGGGCTGGACTGACATCCTCTATAATAACAAACGATGCGCGGCAACACCTG	1135	
Qy	402	rAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCy	422	
Db	1136	GAACTGGCTCTACTTCTCCTCTCATCATCATCGGCTCCTTCTTCATGCTCAACCTGGT	1195	
Qy	422	sLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer-----	438	
Db	1196	GCTGGGGCTGCTCTCGGGGAGTTTGCCAAGGAGCGAGAGGGTGGAGAACCCGCCGCGC	1255	
Qy	439	-----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl	456	
Db	1256	CTTCTGAAGCTGCGCGCAGCAGATCGAG-----	1289	
Qy	456	aSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLe	476	
Db	1290	-----CGAGAGCTCAACGGGTACCTGGAGTGGATCTT	1321	
Qy	476	uArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLe	496	
Db	1322	CAAGCGGAGGAAGTCTATGTCGCGGAGGAGGAC-----	1355	
Qy	496	uLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrAr	516	
Db	1356	-----AGGAATGCAGAGGAGAGTCCCTTTGGACGTGCTGAAGAG	1396	
Qy	516	gSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHi	536	
Db	1397	AGCGGCCCAAGAGAGCAGAAATGACCTGATCCAC-----	1433	
Qy	536	sTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspAr	556	
Db	1434	-----GCAGAGGAGGAGGAGGACCG	1453	
Qy	556	gAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGl	576	
Db	1454	GTTTGCAGAT-----	1463	

QY	576	Y	Gly	Pro	Pro	Arg	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp	Cys	His	Leu	G1	596	
Db	1463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1463	
QY	596	u	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Cys	Pro	Ser	Glu	Ala	Ser	Gly	Arg	Thr	Va	616	
Db	1463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1463	
QY	616	l	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr	Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Ile	Leu	Lys	As	636	
Db	1463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1463	
QY	636	p	Lys	Ala	Leu	Val	Glu	Val	Ala	Pro	Ser	Pro	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Phe	Asn	I1	656	
Db	1463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1463	
QY	656	e	Pro	Pro	Gly	Pro	Phe	Ser	Ser	Met	His	Lys	Leu	Glu	Thr	Gln	Ser	Thr	Gly	Ala	Cy		676	
Db	1463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1463	
QY	676	s	His	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Ser	Lys	Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pr	696	
Db	1464	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1499	
QY	696	o	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg	Thr	Gly	Ala	Gly	Glu	Pro	Glu	Ser	Ala	Asp	His	Va	716	
Db	1500	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1534	
QY	716	l	Met	Pro	Asp	Ser	Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	As	736	
Db	1535	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1535	
QY	736	p	Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	Ala	Glu	Pro	Se		756	
Db	1536	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1550	
QY	756	r	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	Phe	Arg	Lys	Ile	Val	Asp	Ser	Ly	776	
Db	1551	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1588	
QY	776	s	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	Ala	Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	G1	796	
Db	1589	G	A	G	T	T	C	T	A	C	T	T	A	C	T	T	A	C	T	T	A	C	T	1648
QY	796	u	Tyr	His	Glu	Gln	Pro	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Th	816	
Db	1649	G	C	A	T	T	A	C	A	C	C	A	C	C	C	T	G	A	T	T	T	T	1708	
QY	816	r	Ser	Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	Phe	Gly	Tyr	I1	836	
Db	1709	G	G	G	T	C	T	C	T	C	A	C	A	G	A	T	G	T	C	C	T	G	1768	
QY	836	e	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	Ile	Ser	Val	Trp	Glu	Ile	Va		856	
Db	1769	C	G	G	T	C	C	T	T	C	A	A	C	T	G	T	T	G	G	G				

QY 931 pThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheG1 951
 Db 2069 CACA-----ACCAACTTCGACACCTTCCCTGCGCCATCCTCACTGCTTCCA 2116
 QY 951 nIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMet----- 966
 Db 2117 GATCCTGACGGAGAGGACTGGAATGCAGTGATGTATCAGGGATCGAATCGCAAGCGG 2176
 QY 967 -AlaSerThrSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTy 986
 Db 2177 CGTCAGCAAAAGGCATGTTCTCGTCTTTTACTTCAATTGCTTGACACTGTTTCGAAACTA 2236
 QY 986 rValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAl 1006
 Db 2237 CACTCTGTGAATGTCTTTCTGGCCATCGCTGTGGACAACCTGGCCAAACGCCCAAGAGCT 2296
 QY 1006 aThrLysSerGluSerGluProAsp----- 1014
 Db 2297 GACCAAGGATGAAGAGGAGATGGAAGAAGCAGCCAATCAGAAAGCTTGCTCTGC AAAAAGGC 2356
 QY 1015 -----Phe-PheSerProSerValAspGlyA 1023
 Db 2357 CAAAGAAGTGGCTGAAGTCAGCCCCCATGTCTGCCGCGAACAATCTCCATCGCCGCGAGGCA 2416
 QY 1023 spGlyAspArgLysLysArg-LeuAlaLeuValAlaLeuGlyGluHisAla----- 1039
 Db 2417 GCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGGCCAGCCAGTACGGCTGCA 2476
 QY 1040 -----GluLeuArgLysSerLeuLeu-----ProProLeu 1049
 Db 2477 GAACCTGCGGGCCAGCTGCGAGGCGCTGTACAGCGAGATGGACCCCGAGGAGCGGCTGCG 2536
 QY 1050 IleIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGly 1069
 Db 2537 CTTCCGCACTACGCGCCACCTGCGGCCCGACATGAAGACGCACCTTGGACCGCGCGCTGGT 2596
 QY 1070 GluAla-LeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAl 1089
 Db 2597 GGTGGAGCTGGCGCGCGACG 2656
 QY 1089 aAla-----HisHis-----GluMe 1094
 Db 2657 TGCGGAGCCCCCGAGGGCGCTCGACCCCTCCGCGCAGGCAACCGCACCGCGACAAGGA 2716
 QY 1094 tLysCysPro----- 1097
 Db 2717 CAAGACCCCGCGCGGGGACACAGGACCGAGAGGCGCCCGAAGCGGAGAGCGGGGA 2776
 QY 1098 -ProSerAlaArgSerSer-----ProHisSerProTrpSerAlaAlaSerSerTr 1114
 Db 2777 GCCCGGTGCGCGGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG-- 2834
 QY 1114 pThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSe 1134
 Db 2835 ----GGGCCCCCGAGGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2875
 QY 1134 rProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluG1 1154
 Db 2876 CCCCAGGCG 2935
 QY 1154 u-----GluSerSerGluGluAspArgAlaSerPr 1164
 Db 2936 GCCCGGACGCCACCGCGCGCACCGGCACCGAGATCCGAGCAAGGAGTGCGCGCGCGCGCAA 2995
 QY 1164 oAlaGlySerAspHisArgHisArgGlySerLeuGlu-----ArgGluAlaLysSe 1181
 Db 2996 GGGGAGCGAG 3055
 QY 1181 rSerPheAspLeuProAspThrLeuGlnValProGly---LeuHisArgThrAlaSerG1 1200
 Db 3056 CGGG-----GAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAAA 3094
 QY 1200 yArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaSerGlyAr 1218

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 QY 1218 gLeuAla-----ArgThrLeuArgThrAspAspProGlnLe 1230
 Db 3155 GGAGGCTGAGATAGTGAAGCCGACAAAGAAAGGAGCTCCGGAACCAACAGCCCGGGA 3214
 QY 1230 uAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTr 1250
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 QY 1250 pValArgSerArgLeuProAlaCysCysArgGluArg----- 1262
 Db 3261 ----ATGCACACACTGCCCGACACCTGTCTCCAGAAGGTGGAGAAACAGCCAGAGGATGC 3316
 QY 1263 -AspSerTrp----- 1265
 Db 3317 AGACAATCAGCGGAACGTCACCTCGCATGGGCAGTCAGCCCCCAGACCCCGAACACTATTGT 3376
 QY 1265 ----- 1265
 Db 3377 ACATATCCAGTGATGTGTGACGGGCGCCTCTTGGGGGAAGCCACGGTCGTTCCAGTGGTAA 3436
 QY 1265 ----- 1265
 Db 3437 CGTGGACCTGGAAGCCAAAGCAGAGGGGAAGAAAGGAGGTGAAGCGGATGACGTGATGAG 3496
 QY 1266 -----SerAlaTyrIlePheProProGlnSerAr 1275
 Db 3497 GAGCGGCCCCGGCCTATCGTCCCATACAGCTCCATGTTCTGTTAAGCCCCCAACACCT 3556
 QY 1275 gPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuVa 1295
 Db 3557 GCTCCGCGCTTCTGCCCACTACATCGTGACCATGAGGTACTTCCAGGTGGTCTATCTCGT 3616
 QY 1295 lIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe 1315
 Db 3617 GGTATCGCCTTGAGCAGCATCGCCCTGGCTGCTGAGACCCCA---GTGGCGCACAGACTC 3673
 QY 1315 rAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaG1 1335
 Db 3674 GCCAGGAACAACGCTCTGAAATACCTGGATTACATTTTCACTGGTGTCTTTACCTTTGA 3733
 QY 1335 uMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSe 1355
 Db 3734 GATGGTATAAAGATGATCGACTGGGACTGCTGCTTCCACCTGGAGCCTATTTCGGGA 3793
 QY 1355 rSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSe 1375
 Db 3794 CTTGTGGAACATTCTGGAC-----TTCAATTGGTTCAGTGGCGCCCTGGTGGC 3841
 QY 1375 rMetVal---SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLe 1394
 Db 3842 GTTTGCTTCTCAGGATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTCT 3901
 QY 1394 uArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValG1 1414
 Db 3902 TCGTGTCTGCGGCCCCCTCAAGACCATCAAAACGGGCTGCCCAAGCTCAAGGCTGTGTTGA 3961
 QY 1414 uThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePh 1434
 Db 3962 CTGTGTGGTGAACCTCCCTGAAGAATGTCTCAACATCTTGATGTCTACATGCTCTTCAT 4021
 QY 1434 eIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnG1 1454
 Db 4022 GTTCATATTGCCGTCAATGGGTGCAGCTCTTCAAAAGGAAGTTTTCTACTGCACAGA 4081
 QY 1454 yGlu-----AspThrArgAsn-----IleThrAsnLysSerAspCy 1466
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 QY 1466 sAlaGluAlaSerTyrArg---TrpValArgHisLysTyrAsnPheAspAsnLeuGlyG1 1485

Db 4142 AGTGGAAAGCTCAGCCAGGCAGTGGAAAGAAATACGACTTTTCACTACGACAAATGTGCTCTG 4201

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Db 4202 GGCTCTGCTGACGCTGTTACAGTGTCCACGGGAGAAGGCTGGCCCATGGTGTGCTGAAACA 4261

Qy 1505 pGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLe 1525

Db 4262 CTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAGCCCTGGGTACCGCATGGAGCTGTC 4321

Qy 1525 uLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValG1 1545

Db 4322 CATCTTCTACGTGGTCTACTTTGTGGTCTTTCCTTCTTCTTCGTCACACATCTTTGTGGC 4381

Qy 1545 yValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgAr 1565

Db 4382 TTTGATCATCATCACCTTC-----CAGGAGCAGGGGACAAAGGTGAT 4423

Qy 1565 gArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMe 1585

Db 4424 GTCTGAA-----TGCAGCCTGGAGAAGAACGAGAGGGCTTGCACTTGACTTCGC 4471

Qy 1585 tAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArg-----PheArgLeuLe 1603

Db 4472 CATCAGGCCCAACCCCTGACACGGTACATGCCCAAAACCGGCAGTGTTCAGTATAA 4531

Qy 1603 uValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLe 1623

Db 4532 GACGTGGACATTTGTGGTCTCCCGCCCTTTGAATACTTTCATCATGCCCATGATAGCCCT 4591

Qy 1623 uAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLe 1643

Db 4592 CAACACTGTGGTGTGATGATGAAGTTCTATGATGCACCCCTATGATACGAGCTGATGCT 4651

Qy 1643 uLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuVa 1663

Db 4652 GAAATGCCTGAACATCGTGTTCACATCCATCGTGTCTCCATGGAATGCGTGTGAAGATCAT 4711

Qy 1663 lAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleVa 1683

Db 4712 CGCCTTTGGGTGCTGAATATTTCAGAGATGCGTGAATGTCTTTGACTTTGTCACTGT 4771

Qy 1683 lLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu-----ValAs 1698

Db 4772 GTTGGGAAGTATTACTGATATTTTAGTAACAGAGATTGCGGAAACGAAACAATTCATCAA 4831

Qy 1698 nLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1718

Db 4832 CCTCAGC-----TTCTCCGCTCTTTGAGCTGCGCG 4864

Qy 1718 gValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetG1 1738

Db 4865 GCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCATCCTGTCTGGACCTTTGTCCA 4924

Qy 1738 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1758

Db 4925 GTCCCTCAAGGCCCTGCCCTACGTGTGTCTGTCTCATTTGCCATGCTGTCTTCATCATCGC 4984

Qy 1758 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1 1778

Db 4985 CATCATGGGCATGCAGGTGTTGGGAATATTGCCCTGGATGATGAC-----ACCAG 5035

Qy 1778 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1798

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Qy 1816 pGlnGlu-----SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPh 1834

Db 5156 TGACGAGGCCCAATGCCACCGAGTGTGGAAGTACTTTGCCTACTTCTACTTCGTCTCCTT 5215

Qy 1834 eValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet----- 1851

Db 5216 CATCTTCCTGTGCTCCTTTCTGTATGTTGAACCTCTTTGTGGCTGTGATCATGGACAATTT 5275

Qy 1852 -----LysHisLeuGluGlu-SerAsnL 1859

Db 5276 TGAGTACCTCAGCGGGACTCTTCCATCCTAGGTCTCTCACCACTTGGATGAGTTTCATCCG 5335

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Db 5336 GGTCTGGGTGAATACGACCCGGCTGCGTGTGGGCGCATCAGTTACAATGACATGTTTGA 5395

Qy 1879 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVal 1898

Db 5396 GATGCTGAACACATGTCCCGCCTCTGGG-----GCTGGGGAAGAAATGCC 5443

Qy 1899 AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla 1918

Db 5444 TGCTCGAGTTGCTTACAAGCGCCTGGTTGCG--CATGAACATGCCCATCTCCAACGAGGA 5500

Qy 1919 SerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValPro 1938

Db 5501 CATGACTGTTCACTTCAGCTCCACGCTGATGGCCCTCATCCGACGCGCACTGGAGATCAA 5560

Qy 1939 LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958

Db 5561 GCTGGCCCCAGCTGG-----GACAAAGCAGCATCATGTGTACGCGGAGTTGAG 5608

Qy 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGly----- 1975

Db 5609 GAAGGAGATTTCCGTTGT---GTGGGCCAATCTGCCCCAGAAAGACTTGTGACTTGTGTTGT 5665

Qy 1976 -----HisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1987

Db 5666 ACCACCCCATAAAGCTGATGAGATGACAGTGGGGAAGTTTATGCAGCTCTGATGATAATT 5725

Qy 1988 SerIleLeuSerVal-----HisSerGlnPro----- 1996

Db 5726 TGACTTCTACAAGCAGAAACAAACCACCAAGACCATGATGCAGAGCTCTGGAGGCCT 5785

Qy 1997 ---AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnPro 2015

Db 5786 CTCCCAGATGGGTCTGTGTCCCTGTTCCACCCTCTGAAGGCCAC----- 5830

Qy 2016 HisGlyAlaProThrTrpGlyAlaIleProLysLeuPro----- 2028

Db 5831 CCTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGCCCGGTTTCTTCGACAGAAAGAG 5890

Qy 2028 ----- 2028

Db 5891 TTCCACCTCCCTCAGCAATGGCGGGGCCCATACAAAACCAAGAGAGTGGCATCAAAGAGTC 5950

Qy 2029 -----ProProGly 2031

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Qy 2032 ArgSerProLeu-AlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp----- 2049

Db 6011 GCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTGAGGAGCACTGGCTGTGGACGTTCA 6070

Qy 2050 -----SerLeuAspValG1 2054

Db 6071 GATGCAGAGCATAAACCGGAGGGGCCCTGATGGGGAGCCCCAGCCTGGGCTGGAGAGCCA 6130

Qy 2054 nGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro-----SerCy 2071

Db 6131 GGGTTCGAGCGGCCTCCATGCCCGCCTTGCGGCCGAGACTCAGCCCGTCACAGATGCCAG 6190

Qy 2071 sProLeuThrArgSerSerPheTrpGlyGlySerIleGlnValGlnArgSe 2091

Db 6191 CCCCATGAAGCGCTCCATCTCC-----ACGCTGGCCCGAGCGGCC 6229

QY 2091 rGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeu-- 2110
Db 6230 CCGTGG-GACTCATCTTTGCAGCACCAACCCCGGACCGCCACCCCTAGCCAGCGCTCGT 6288
QY 2111 ----GluProSerTrpAlaLysAspProProGlu-ThrArgSerSerLeuGluLeuAspT 2129
Db 6289 CGCACCAACCAACCAACCGCTGCCACCGCCGCGAGGACAGGAAGCAGAGTCCCTGGAGA 6348
QY 2129 hrGluLeuSerTrpIleSerGlyAspLeu-----LeuProSerSerGlnGluProL 2147
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QY 2147 euPhePro-----ArgAspLeuLysLysCysTyrSerV 2158
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QY 2178 erileAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSer- 2197
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QY 2197 ----- 2197
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QY 2198 -----SerLeuGlyGlyGlnProLeu-----G 2205
Db 6637 GTGGTTCGTGAATGGGAGGCCCTTGCTGTCAACATCTGGTGTAGCACCCCGCGCGG 6696
QY 2205 lyGlyProGlySerArgProLysLysLysLeuSerPro---ProSerIleSerIleAspP 2224
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Db 6817 CAGGCGGCTCAGCGCTGGGCTTTCCGAACACAAACGCCCTGTGCAGAGAGACCCCTCA 6876
QY 2247 erAsp-----SerLysAspProSerValSerSerProLeuA 2259
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QY 2259 spSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeu----- 2274
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QY 2275 -----SerGlyLeuSerSer 2279
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RESULT 15
US-08-193-078B-7
; Sequence 7, Application US/08193078B
; Patent No. 5846757
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
; STREET: 1660 UNION STREET

CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..7163
NAME/KEY: 5'UTR
LOCATION: 1..143
NAME/KEY: 3'UTR
LOCATION: 7161..7362
US-08-193-078B-7
Alignment Scores:
Pred. No.: 2.92e-96 Length: 7362
Score: 1745.50 Matches: 662
Percent Similarity: 37.80% Conservative: 356
Best Local Similarity: 24.58% Mismatches: 879
Query Match: 14.51% Indels: 798
DB: 2 Gaps: 84
US-09-611-257A-24 (1-2287) x US-08-193-078B-7 (1-7362)
QY 14 ProLeuArgGlySerAlaArgProSerSerAspProGlyProArgLeuAlaArgGly 33
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QY 34 TrpThrArg-ArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerAr 53
Db 123 TGCACGCGGGGCGCGGAGCCATGTCCTCGGGGACGAGCTGGCGCGCGCTATGGA 182
QY 53 gSerSerThrCysProGlyProGlyAlaAlaGly---AlaGlySerThrGluLysAs 72
Db 183 GGCCCCGGCGGAGAGCGGGCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGGT 242
QY 72 pProGlySerAlaAspSerGluAlaGluGlyLeu----- 83
Db 243 CCGGGGGGCTGC---AGCCCGCCAGCGGGTCTCTACAAGCAATCGATCGCGCAGCGC 299
QY 84 -----ProTyrProAlaLeuAlaProVal----- 91
Db 300 GCGCGGACCATGGCGCTGTACAAC-CCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 358

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Db 359 CCGCTCGCTCTTGGTCTTTCAGCGAGGACAACGTCGTCCGCAATACGGCAAGCGCATCAC 418
Qy 110 lCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLe 130
Db 419 CGAGTGGCCTCCATTCGAGAATATGATCCTGGCCACCATCATCGCCAACTGCATCGTGCT 478
Qy 130 uGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGl 150
Db 479 GGCCCTG-----GAGCAGCACCTCCCTGATGGGACAAAACGCCCATGTCCGA 526
Qy 150 nAlaPheAspAsp-----PheIlePheAlaPhePheAlaValGluMetValVally 167
Db 527 GCGGCTGGACGACACGGAGGCCCTATTTCATCGGGATCTTTTGCTTCGAGGCAGGATCAA 586
Qy 167 sMetValAlaLeuGly---IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnAr 186
Db 587 AATCATCGCTCTGGGCTTTGTCTTCCACAAGGGCTCTTACCTGCCGAACGGCTGGAACGT 646
Qy 186 gLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAspLe 203
Db 647 CATGGACTTCGTGGTGCCTCCTCACAGGGATCCTTGCCACGGCTGGAACTGACCTTCGACCT 706
Qy 203 uGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaI1 223
Db 707 GCGA-----ACACTGAGGGCTGTGGTGTGTGAGGCCCTGAAGCTGGT 751
Qy 223 eAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLe 243
Db 752 GTCTGGGATTCCAAGTTTGCAAGTGGTGTGCTCAAGTCCATCATGAAGGCCATGTTTCCACT 811
Qy 243 uGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGl 263
Db 812 CCTGCAGATTGGGCTGCTTCTTCTTTGCCATCCTCATGTTTGCCATCATTTGCCCTGGA 871
Qy 263 nLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLe 283
Db 872 GTTCTACATGGGCAAGTTCACAAGGCCTGTTTC-----CCCAA 910
Qy 283 uSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPropheIleCy 303
Db 911 CAGCACAGATGGGAGCCCGTG----- 932
Qy 303 sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl 323
Db 932 ----- 932
Qy 323 uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsnTh 343
Db 933 -----GGTGACTTCCCTGTGGCAAGGAGGCCCCAGCCGGCTGTGCGAGGCGACAC 985
Qy 343 rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPh 363
Db 986 TGAGTGC-----CGGGAGTACTGGCCA-----GGACCCAA 1015
Qy 363 eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValI1 383
Db 1016 CTTTGGCATCACCAACITTGACAATATCCTGTGTGCCATCTTGACGGTGTTCAGTGCA 1075
Qy 383 eThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp----AlaHisSerPheTy 402
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Qy 402 rAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCy 422
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Qy 422 sLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer----- 438
Db 1196 GCTGGGCGTGCTCTCGGGGAGTTTGGCAAGGAGCGAGAGGGGTGGAGAACCGCGCGC 1255
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Qy 439 -----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl 456
Db 1256 CTTCCTGAAGCTGCGCCGCGCAGCAGCAGATCGAG----- 1289
Qy 456 aSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLe 476
Db 1290 -----CGAGAGCTCAACGGGTACCTGGAGTGGATCTT 1321
Qy 476 uArgLysAlaIaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLe 496
Db 1322 CAAGGGCGGAGGAAGTCACTGCTGGCCGAGGAGGAC----- 1355
Qy 496 uLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrAr 516
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Qy 516 qSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisH1 536
Db 1397 AGCGGCCACCACAAGAAAGAGCAGAAATGACCTGATCCAC----- 1433
Qy 536 sTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspAr 556
Db 1434 -----GCAGAGGAGGAGGAGACCG 1453
Qy 556 gAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGl 576
Db 1454 GTTTGCAGAT----- 1463
Qy 576 yGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGl 596
Db 1463 ----- 1463
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Qy 616 lGlySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAs 636
Db 1463 ----- 1463
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Db 1463 ----- 1463
Qy 656 eProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCy 676
Db 1463 ----- 1463
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Db 1464 -----CTCTGTGCTGTGGATCCCTTCGCCCGCCGACG----- 1499
Qy 696 oAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVa 716
Db 1500 -----CTCAAGAGCGGGAAGACAGAGAGCTCGTCATACTT 1534
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Db 1535 C----- 1535
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Qy 756 rSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLy 776
Db 1551 -----ATGTTCCGGTTTT-----ATCCGGCGCATGGTGAAGGCTCA 1588
Qy 776 sTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGl 796
Db 1589 GAGCTTCTACTGGGTGGTGTCTGTGCTGGTGGCCCTGAACACACTGTGTGTGGCCATGGT 1648
Qy 796 uTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheTh 816
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 QY 816 rSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrI1 836
 Db 1709 GGGTCTCTCTCACAGAGATGCTCCCTGAAGATGTATGGCCTGGGGCCCAAGACTACTT 1768
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11980	99.6	6942	18	US-10-377-139-7 Sequence 7, Appli
2	11829	98.3	7285	10	US-09-383-894-3 Sequence 3, Appli
3	11673	97.0	7129	10	US-09-383-894-1 Sequence 1, Appli
4	10845.5	90.2	7648	18	US-10-377-139-10 Sequence 10, Appl
5	10845.5	90.2	7648	18	US-10-757-262-15 Sequence 15, Appl
6	10707	89.0	8116	17	US-10-062-674-2011 Sequence 2011, Ap
7	6103	50.7	3993	19	US-10-930-301-51 Sequence 51, Appl
8	5432.5	45.2	6990	18	US-10-377-139-8 Sequence 8, Appli
9	5420	45.1	6816	9	US-09-935-541-1 Sequence 1, Appli
10	5420	45.1	6816	16	US-10-425-800-1 Sequence 3, Appli
11	5420	45.1	6855	9	US-09-935-541-3 Sequence 3, Appli
12	5420	45.1	6855	16	US-10-425-800-3 Sequence 3, Appli
13	5407	45.0	6503	9	US-09-935-541-12 Sequence 12, Appl
14	5407	45.0	6503	16	US-10-425-800-12 Sequence 12, Appl
15	3950	32.8	5562	9	US-09-030-482B-18 Sequence 18, Appl
16	3861.5	32.1	6073	18	US-10-377-139-11 Sequence 11, Appl
17	1745.5	14.5	7362	17	US-10-375-253-11 Sequence 11, Appl
18	1743.5	14.5	7376	13	US-10-033-026-3 Sequence 3, Appli
19	1739.5	14.5	7364	9	US-09-954-456-1179 Sequence 1179, Ap
20	1739.5	14.5	7364	13	US-10-033-026-5 Sequence 5, Appli
21	1739.5	14.5	7364	18	US-10-736-883-31 Sequence 31, Appl
22	1739.5	14.5	7364	19	US-10-843-641A-4206 Sequence 4206, Ap
23	1732.5	14.4	6984	18	US-10-736-883-37 Sequence 37, Appl
24	1727	14.4	7175	17	US-10-375-253-13 Sequence 13, Appl
25	1726.5	14.4	7121	18	US-10-736-883-43 Sequence 43, Appl
26	1725	14.3	7185	18	US-10-736-883-39 Sequence 39, Appl
27	1721	14.3	7177	13	US-10-033-026-7 Sequence 7, Appli
28	1721	14.3	7177	18	US-10-736-883-33 Sequence 33, Appl
29	1720.5	14.3	6792	17	US-10-627-370-1 Sequence 1, Appli
30	1720	14.3	9695	18	US-10-736-883-27 Sequence 27, Appl
31	1720	14.3	9695	19	US-10-486-706-207 Sequence 207, App
32	1717.5	14.3	6083	13	US-10-029-413A-21 Sequence 21, Appl
33	1716.5	14.3	7713	18	US-10-736-883-41 Sequence 41, Appl
34	1693	14.1	7011	13	US-10-033-026-9 Sequence 9, Appli
35	1693	14.1	7011	18	US-10-736-883-29 Sequence 29, Appl
36	1686	14.0	7348	18	US-10-322-696-175 Sequence 175, App
37	1685.5	14.0	7291	18	US-10-322-696-83 Sequence 83, Appl
38	1685.5	14.0	7477	18	US-10-322-696-177 Sequence 177, App
39	1684.5	14.0	6572	18	US-10-467-491-1 Sequence 1, Appli
40	1682.5	14.0	7363	18	US-10-723-860-5192 Sequence 5192, Ap
41	1675.5	13.9	6503	18	US-10-377-139-16 Sequence 16, Appl
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43	1671	13.9	7032	17	US-10-375-253-37 Sequence 37, Appl
44	1667	13.9	9704	18	US-10-322-696-80 Sequence 80, Appl
45	1665.5	13.8	8490	15	US-10-101-510-617 Sequence 617, App

ALIGNMENTS

RESULT 1
US-10-377-139-7
; Sequence 7, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-377-139-7

Alignment Scores:

Pred. No.: 0 Length: 6942
Score: 11980.00 Matches: 2283
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 3
Query Match: 99.60% Indels: 2
DB: 18 Gaps: 0

US-09-611-257A-24 (1-2287) x US-10-377-139-7 (1-6942)

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Qy	21	ProSerSerAspProProGlyProArgLeuAlaArgGlyTirPThrArgArgArgMetGlu	40
Db	76	CCCTCTTCGGACCCCGGGGCCCCGGCTGGCCAGAGGATGGACGAGGAGGATGGAG	135
Qy	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly	60
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Qy	61	ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluA	80
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Qy	100	erArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerM	120
Db	316	GCCTCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAACCCCGTGGTTCGAGCGAGTCA	375
Qy	120	etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA	140
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Qy	140	laCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPheP	160
Db	436	CCTGTGACTCCCGAGCTGCCGATCCTGCGAGCCTTCGATGACTTCATCTTTGCCTTCT	495
Qy	160	heAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrL	180
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Qy	180	euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS	200
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Qy	420	snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL	440
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Qy	620	ysValTyrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuV	640
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Db 2656 TCCTGCCGCCCTGCAGCGCCAGTCTGGTGTCTCATGAAGACCATGGACAACGTGGCCA 2715

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QY 1600 heArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyV 1620
Db 4816 TCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTTCATCACTGGTG 4875
QY 1620 alIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA 1640
Db 4876 TCATCGGGCTGAACGTGTGCTACTATGGCCATGGAACTTACCAGCAGCCCCAGATCCTGG 4935
QY 1640 spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP 1660
Db 4936 ACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTTCATCTTTGTCTTTGAGTCAGTTT 4995
QY 1660 heLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAspL 1680
Db 4996 TCAAACTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGGAACAGCTGGACC 5055
QY 1680 euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS 1700
Db 5056 TGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGT 5115
QY 1700 erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL 1720
Db 5116 CGTGGCCCATCAACCCCAACCATCATCCGTATCATGAGGGTGCTCCGCATGTCTCGAGTTC 5175
QY 1720 euLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL 1740
Db 5176 TGAAGCTGTTGAAGATGGCTGTGGGCATGGGGCACTGCTGCACACCGTGTATGCAGGCC 5235
QY 1740 euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheAlaAlaL 1760
Db 5236 TGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTATTGTTTTCATCTTTTCAGCTC 5295
QY 1760 euGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG 1780

Db 5296 TGGGCGTGGAGCTCTTTGGAGACCTTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGG 5355
QY 1780 lyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT 1800
Db 5356 GTCGGCATGCCACCTTTAGGAACCTTTGGTATGGCCTTTCTGACCCTCTCTCCGAGTCTCCA 5415
QY 1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT 1820
Db 5416 CTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCA 5475
QY 1820 hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP 1840
Db 5476 CCTGCTACAACACTGTTCATCTCCCTATCTACTTTGTGTCTTCTGCTGACGGCCCACT 5535
QY 1840 heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysG 1860
Db 5536 TTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTTGAAGAAAGCAACAAG 5595
QY 1860 luAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuSerP 1880
Db 5596 AGGCCAAGGAGGAGCGGAGCTCGAGGCGGAGCTGGAGCTGGAGATGAAGACGCTCAGCC 5655
QY 1880 roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS 1900
Db 5656 CGCAGCCCCACTCCCGCTGGGCAGCCCTTCTCTGGCCCGGGTGGAGGTGTCAACA 5715
QY 1900 erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG 1920
Db 5716 GTACTGACAGCCCTAAGCCTGGGCTCCACACACCACTGCCCCACATTGGAGCAGCCTCGG 5775
QY 1920 lyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG 1940
Db 5776 GCTTCTCCTTGAGCACCCACCATGTGTACCCACCCCGAGGAGTGCCAGTCCCCCTAG 5835
QY 1940 lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA 1960
Db 5836 GACCAGACCTGTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCCCAATG 5895
QY 1960 spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG 1980
Db 5896 ACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGCTGGG 5955
QY 1980 lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS 2000
Db 5956 GGCTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACACGACAGACCA 6015
QY 2000 erCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProT 2020
Db 6016 GCTGCATCCTACAGCTTCCAAAGATGTGCATATCTGTCTCCAGCCTCATGGGCTCCCA 6075
QY 2020 hrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProL 2040
Db 6076 CCTGGGCGCCATCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGGCCTC 6135
QY 2040 euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG 2060
Db 6136 TCAGGCGCCAGGCAGCAATAAGGACTGCTCCCTGGATGTGCAGGGCTGGGTAGCCGGG 6195
QY 2060 luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT 2080
Db 6196 AAGACCTGTTGTACAGAGTGAGTGGGCCCTCTGTCCTCTGACCCCGGTCTCATCTTCT 6255
QY 2080 rpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysH 2100
Db 6256 GGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAAGTCTCCAAGC 6315
QY 2100 isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG 2120
Db 6316 ACATCCGCTGCCAGCCCTTGCCAGGCCTGGAACCCAGCTGGGCCAAGGACCCCTCCAG 6375
QY 2120 luThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeup 2140

6376	AGACCAGAACGACGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTTCAGGAGACCTCCTTC	6435
2140	roSerSerGlnGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluT	2160
6436	CCAGCAGCCAGGAAGAACCCCTGTTCCACGGGACCTGAAGAAGTGTCTACAGTGTAGAGA	6495
2160	hrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleA	2180
6496	CCCAGAGCTGCAGGCGCAGGCCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTG	6555
2180	laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG	2200
6556	CTGTCTAGCTGTCTGGACAGGGCTCCCAACCCCGGCTATGTCCAAGCCCTCAAGCCTCG	6615
2200	lyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerI	2220
6616	GGGGCCAACTCTTGGGGTCTCTGGGAGCCGGCCTAAGAAAAAACTCAGCCCAACCCAGTA	6675
2220	leSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysL	2240
6676	TCTCTATAGACCCCGAGAGCCAGGGCTCTCGGGCCCCCATGCAGTCTCTGGTGTCTGCC	6735
2240	euArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspS	2260
6736	TCAGGAGGAGGGCGCGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACA	6795
2260	erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSera	2280
6796	GCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTG	6855
2280	spProThrAspMetAspPro	2286
6856	ACCCAACAGACATGGACCCC	6875

RESULT 2

US-09-383-894-3
; Sequence 3, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-3

Alignment Scores:		
Pred. No.:	0	Length: 7285
Score:	11829.00	Matches: 2270
Percent Similarity:	97.72%	Conservative: 1
Best Local Similarity:	97.68%	Mismatches: 15
Query Match:	98.35%	Indels: 38
DB:	10	Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-383-894-3 (1-7285)

Qy		1 MetLeuProHisArg-ValProArg-CysValAlrGThrProProLeuArgGlySerAlaa	20
Dd			
		57 ATGCTCCCCCACCGGGTCCCCCGGTTCGTAGGACACTCCTCTGAGGGGCTCCGCTC	116
Qy		20 rgProSerSerAspProGlyProArgLeualaArgGlyTrpThrArgArgMetG	40
Dd			
		117 GCCCTCTTCGGACCCTCCGGGCCCGGGTGCGGCAGAGGATGGACGAGGAGGAGATTG	176

Qy 399 sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPheMetI 419
 Db 1257 CTCCTTCTACAACTCATCTACTTCTCATCTCATCTCGTGGCTCCTTCTCATGAT 1316
 Qy 419 eAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG1 439
 Db 1317 CAACCTGTGCTGGTGGTATTGCCACGCGAGTTCTCCGAGACCAACAGCGGGAGAGTCA 1376
 Qy 439 nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459
 Db 1377 GCTGATCGGGAGCAGCGTGTACGATTCTCTGTCCAATGCTAGCACCTGGCAAGCTTCTC 1436
 Qy 459 rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl 479
 Db 1437 TGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCTCCGAAAAGC 1496
 Qy 479 aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499
 Db 1497 AGCCCGAAGGCTGGCCAGGCTCTTAGGGCTATAGGCGTGCAGGCTGGGCTGCTCAGCAG 1556
 Qy 499 rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr 519
 Db 1557 CCCAGTGGCCCGTAGTGGCAGGAGCCCCAGCCAGTGGCAGCTGCACCTCGCTCACACCG 1616
 Qy 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrHisLe 539
 Db 1617 TCGTCTGTCTGCCACACCTGGTCCACCACCATCACCACTACCACTACCACT 1676
 Qy 539 uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAlaAs 559
 Db 1677 GGGTAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGACAGGGATGCCAA 1736
 Qy 559 nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr 579
 Db 1737 TGGGTCTCGCCGGCTCATCTACCACCACTCTACCCACTCCCTCTGGGGCCCTCC 1796
 Qy 579 oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr 599
 Db 1797 GAGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCG 1856
 Qy 599 qCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerG1 619
 Db 1857 TTGCCAGGACCCCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTG 1916
 Qy 619 yLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe 639
 Db 1917 GAAGGTGTACCCCACTGTGCATACCAAGCTCCAGCCCTCCACAGAGATACTGAAGGATAAAGCACT 1976
 Qy 639 uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG1 659
 Db 1977 AGTGGAGGTGGCCCCCAGCCCTGGGCCCTCCACCCCTCACCAGCTTCAACATCCCACCTGG 2036
 Qy 659 yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe 679
 Db 2037 GCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTACGGGAGCCTGCCATAGCTC 2096
 Qy 679 rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy 699
 Db 2097 CTGCAAAATCTCCAGCCCTGTCTCCAAGGCAGAGTGGAGCCTGCGGCGCGGACAGTTG 2156
 Qy 699 sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs 719
 Db 2157 TCCCTACTGTGCCGGACAGGAGCAGGAGCGCAGAGTCCGCTGACCATGTATGCCTGA 2216
 Qy 719 pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs 739
 Db 2217 CTCAGACAGCGAGGCTGTGTATGAGTTTCCACAGGACGCTCAGCACAGTACCTCCGGGA 2276
 Qy 739 pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle 759
 Db 2277 TCCCCACAGCCGGCGGACAGCGGAGCCCTGGGCCAGATGCAGAGCTAGTTCTGTGCT 2336
 Qy 759 uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG1 779

Db 2337 GGCTTTCTGGAGGCTGATCTGTGACACATCCGGAAGATCGTAGATAGCAATACITTTGG 2396
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 Db 2397 CCGGGAAATCATGATCGCCATCCTGGTCAATACACTCAGATGGGCATCGAGTACCACGA 2456
 Qy 799 uGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh 819
 Db 2457 GCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTTACCAGCCTCTT 2516
 Qy 819 eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnPr 839
 Db 2517 CGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTTGGCTACATTAAGAAATCC 2576
 Qy 839 oTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnG1 859
 Db 2577 CTACAACATCTTTGATGGTGTCTATTGTGTCATCAGTGTGGAGATTGTGGGCCAGCA 2636
 Qy 859 nGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr 879
 Db 2637 GGGAGGTGGCCTGTTCGGTGTTCGGACCTTCCGCCCTGATCGCGTGTCTGAAGCTGGTGG 2696
 Qy 879 qPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl 899
 Db 2697 CTTCTCTCCCGCCCTGCAGCGCCAGCTCGTGGTGTCTCATGAGACCATGGACAACGTGGC 2756
 Qy 899 aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe 919
 Db 2757 CACCTTCTGCATGCTCCTCATGCTGTTCATCTTTCATCTTTCAGCATCCTGGGCATGCATCT 2816
 Qy 919 uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh 939
 Db 2817 CTTTGGTTGCAAGTTTCGATCTGAACGGGATGGGACACCGTTGCAGACCGGAAGAAATTT 2876
 Qy 939 eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs 959
 Db 2877 CGACTCCCTGCTTGGGCCATCGTCACTGTCTTTTCAGATTCTGACTCAGGAAGACTGGAA 2936
 Qy 959 nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl 979
 Db 2937 TAAAGTCTCTTACAACGGCATGGCCCTCCACATCGTCTTGGGCTGTCTTTACTTCATCGC 2996
 Qy 979 aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG1 999
 Db 2997 CCTCATGACTTTTGGCAACTATGTGCTCTTTAACTTGTGGTGGCCATTCTTGTGAAGG 3056
 Qy 999 yPheGlnAlaGlu----- 1003
 Db 3057 ATTCCAGGCAGAGGAAATCGCAAAACGGGAAGATGCGAGTGGACAGTTAAGCTGTATTCA 3116
 Qy 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePh 1016
 Db 3117 GCTGCCTGTCAACTCTCAGGGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTT 3176
 Qy 1016 eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuG1 1036
 Db 3177 TTCGCCCATGTGGATGGTGTATGGGACAGAAAGACGCGCTTGGCCCTGGTGGCTTTGGG 3236
 Qy 1036 yGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaTh 1056
 Db 3237 AGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCATACGGCTGCGAC 3296
 Qy 1056 rProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe 1076
 Db 3297 ACCAATGTCACTACCAAGAGCTCCAGCAGGTTGTGGGGAAGCACTGGGCTCTGGCTC 3356
 Qy 1076 rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy 1096
 Db 3357 TCGACGTACCACTAGCAGTGGGTCCCGCTGAGCCTGGAGCTGCCCATGAGATGAAATC 3416
 Qy 1096 sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1116

Db 3417 TCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGGCGCAAGCAGCTGGACCAG 3476

QY 1116 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1136

Db 3477 CAGGCGCTCCAGCAGGAACAGCCTGGGCGGGCCCCCAGCCTAAAGCGGAGGAGCCGAG 3536

QY 1136 rGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlnSerGlnAspGluGluGluse 1156

Db 3537 CGGGGAGCGGAGGTCCCTGCTGCTGGAGAGGGCCAGGAGAGTCAGGATGAGGAGGAAAG 3596

QY 1156 rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuG1 1176

Db 3597 TTCAGAAAGAGGACCGGGCCAGCCCGCAGGCGAGTGACCATGCCACAGGGGTTCCTTGA 3656

QY 1176 uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr 1196

Db 3657 ACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCGGGCTGCACCG 3716

QY 1196 gThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlase 1216

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QY 1236 nAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPr 1256

Db 3837 TGATGAGGGAATCTGAGCAAAAGGGAACGCATACAAGCTGGGTGAGATCCCGGCTTCC 3896

QY 1256 oAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPh 1276

Db 3897 TGCCTGTTGCCGAGAGCGAGATTCTGGTCGGCCTATATCTTCTCCTCAGTCAAGGTT 3956

QY 1276 eArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValI1 1296

Db 3957 TCGTCTCCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTGGTCCTCGTCAT 4016

QY 1296 eIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAl 1316

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Db 4077 TGAGCGCATCTTCTGACCCCTCTCCAACATACATCTTCACGCGAGTCTTTCTAGTGAAAT 4136

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Db 4137 GACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTACCTGGCAGCAG 4196

QY 1356 rTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMe 1376

Db 4197 CTGGAATGTCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATCCTGGTCTCCAT 4256

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QY 1416 uMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleI1 1436

Db 4377 GATGTCACTCCCTCAAA CCCATTGGCAACATTGTGGTCATTGTGTGTCCTTCTCATCAT 4436

QY 1436 ePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAs 1456

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QY 1476 sLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLy 1496

Db 4557 CAAGTACAAACTTTGACAAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTGTGGCTTCCAA 4616

QY 1496 sAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPr 1516

Db 4617 GGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTGGATCAGCAGCC 4676

QY 1516 oIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAl 1536

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QY 1556 nHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLy 1576

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Db 4857 AAAGAGAAGGAATCTAATGTTGGACGATGTAATTGCTCCGGCAGCTCAGCCAGCGCTGC 4916

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Db 4917 GTCAGAAGCCCAAGTGCAGGCCCTACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCA 4976

QY 1605 sHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVa 1625

Db 4977 CCACCTGTGTACCGCCACTACTCGACCTCTTTCATCATGGTGTTCATCGGGCTGAACGT 5036

QY 1625 lValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysI1 1645

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QY 1685 uSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnPr 1705

Db 5217 GTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATGCTTCGCTGCCCATCAACCC 5276

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Db 5517 TAGGAACCTTGGTATGGCCCTTCTGACCCCTCTTCCGAGTCTCCACTGGTGACAACTGGAA 5576

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Db 5577 TGGTATTATGAAGGACACCCCTCCGGGACTGTGACCAAGGAGTCCACCTGCTACACACTGT 5636

Qy 1825 lIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVa 1845
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Db 5757 CGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCGCGAGCCCCACTCCCC 5816
Qy 1885 oLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLy 1905
Db 5817 GCTGGGCAGCCCTTCTCTGGCCCGGGGTGGAGGGTGTCAACAGTCTCTGACAGCCCTAA 5876
Qy 1905 sProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHi 1925
Db 5877 GCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCA 5936
Qy 1925 sProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh 1945
Db 5937 CCCACGATGGTACCCACCCCGAGGAGGTGCGAGTCCCCCTAGGACCAAGACCTGCTGAC 5996
Qy 1945 rValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysAr 1965
Db 5997 TGTGAGGAAGTCTGGTGTcAGCCGGACGCACTCTCTGCCCCAATGACAGCTACATGTGCCG 6056
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Db 6057 CAATGGGAGCACTGCTGAGATCCCTTAGGACAGGGGTGGGGCTCCCCAAAGCCCCA 6116
Qy 1985 nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLe 2005
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Qy 2005 uProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePr 2025
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Db 6237 TAAACTACCCCCACCTGGCCCGCTCCCCCTCTGGCTCAGAGGCCTCTCAGCGCCAGGCAGC 6296
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Qy 2105 aProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLe 2125
Db 6477 CCCTTGCCAGGCCCTGGAACCCAGCTGGGCCAAGGACCTCCAGAGACCAGAACAGCAGCTT 6536
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US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7129
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-1
Alignment Scores:
Pred. No.: 0 Length: 7129
Score: 11673.00 Matches: 2237
Percent Similarity: 97.77% Conservative: 1
Best Local Similarity: 97.73% Mismatches: 15
Query Match: 97.05% Indels: 36
DB: 10 Gaps: 2
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Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGCAGCGCGGACTCCGAGCGGAGGGGCTCCGTACCCGGCGCTAGCCCGGTGTTT 181
Qy 93 hepheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCCGCCCGGAGCTGGTGTCTCCGACCGGTCTGTAACC 241
Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetp 133

Db 242 CGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATGT 301

Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153

Db 302 TCAGGCCGTGTGAGGACATTGCTGTGACTCCAGCGCTCCGGATCCTGCAGGCCTTCG 361

Qy 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTGCCCTTCTTTGCTGTGAAATGGTGGTGAAGATGGTGGCTTGGCA 421

Qy 173 lePheGlyLysCysTyrLeuGlyAspThrTirAsnArgLeuAspPheIleValI 193

Db 422 TCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACGGCTTGACTTTTTCATTGTCA 481

Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213

Db 482 TTGCAGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCGAGTCAGGA 541

Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGGTGGCCAGCATGCGCATTCG 601

Qy 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253

Db 602 TCACATTACTGCTGGACACCTTGCTATGCTGGCAACCTCCTGCTGCTCTCTCTTCG 661

Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTirAlaGlyLeuLeuArgAsnArgC 273

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Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgs 313

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Qy 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333

Db 842 CCTGCAGGAGTGTCCACACTGCTGGGGAAGCGGTGGTGGCCCCACCCCTGCAGTCTGG 901

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Db 962 CCAACTGCTCTGCGGGCGAGCAACAACCCCTTCAAAGGCGCCATCAACTTTTGACAACATTG 1021

Qy 373 lyTyrAlaTirPilleAlaIlePheGlnValIleThrLeuGluGlyTirPValAspIleMetT 393

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Db 1502 ACCATCACCACTACCACTGGGTAATGGACGCTCAGAGTTCCCGGGCCAGCCAGAGA 1561

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Db 1742 GTAGGACTGTGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAGA 1801

Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653

Db 1802 TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCCTCACCA 1861

Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673

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Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693

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Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713

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Qy 753 laGluProSerSerValLeuAlaPheTirPArgLeuIleCysAspThrPheArgLysIlev 773

Db 2162 CAGAGCTAGTTCTGTGTGCTGCTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATCG 2221

Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793

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Db 2342 TCGTCTTCACCAGCCTCTTCGCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCT 2401

Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853

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QY 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639

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RESULT 4
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; Sequence 10, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-10

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservative: 33
Best Local Similarity: 88.33% Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 18 Gaps: 7

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Qy 1659 alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA 1679
Db 4976 TTTTCAAACCTTGTGGCCTTTGGTTTCCGTCGGTCTCTTCCAGACAGGTGGAACCCAGCTGG 5035
Qy 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5036 ACCTGGCCATTGTGCTGCTGTCCATCATGGGCATCACGCTGGAGAAATCGAGGTCAACG 5095
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5096 CCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTGCGCATTGCCCGAG 5155
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5156 TGCTGAAGCTGCTGAAGATGGCTGTGGCATGCGGGCGCTGCTGGACACGGTGATGCAGG 5215
Qy 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
Db 5216 CCGTGGCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGCAG 5275
Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5276 CTCTGGCGCTGGAGCTCTTTGGAGACCTGGAGTGTACGAGACACACCCCTGTGAGGGCC 5335
Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals 1799
Db 5336 TGGCGCGTCATGCCACCTTTCGAACTTTGGCATGGCCTTCTTAACCTCTTCCGAGTCT 5395
Qy 1799 erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5396 CCACAGGTGACAAATTGGAATGGCATTTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGT 5455
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5456 CCACCTGTCTACAAACACGCTCATCTCGCCTATCTACTTTGTGTCCTTCTGTCGTGACGGCCC 5515
Qy 1839 lnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluMetLysThrLeuS 1859
Db 5516 AGTTCGTGCTAGTCAACGTGGTGTATCGCCGTGTGTATGAAGCACCTGGAGGAGAGCAACA 5575
Qy 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuS 1879
Db 5576 AGGAGGCCAAGGAGGAGGCGGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCA 5635
Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
Db 5636 GCGCCCGAGCCCACTCGCCACTGGGCGAGCCCTTCTCTCTGGCTGGGGTTCGAGGGCCCGG 5695
Qy 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS 1919
Db 5696 ACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACCGAGATCAGCCT 5755
Qy 1919 erGlyPheSerLeuGluHisProThr----- 1927
Db 5756 CCCACTTTTCCCTGGAGCACCCACCGGACAGGCAGCTGTTTGACACCATATCCCTGCTGA 5815
Qy 1927 ----- 1927
Db 5816 TCCAGGGCTCCCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGSCAGGCCCCAGGGGCC 5875
Qy 1927 ----- 1927
Db 5876 AGCCCTCTGCCCTTCCCTTCTGCCCCCCAGCCTGGAGGCTCCGACCCACAGATCCCTCTAG 5935
Qy 1927 ----- 1927
Db 5936 CTGAGATGGAGGCTCTGTCTCTGACGTACAGAGATTGTGTCTGAACCGTCTGTCTCTCTAG 5995
Qy 1927 ----- 1927

Db 5996 CTCTGACGGATGACTCTTTGGCCTGATGACATGCACACTCTTACTTAGTGCCCTGGAGA 6055

Qy 1928 -----MetValProHisProGluValProValProLeuGlyProAspLeuLeuThrV 1946

Db 6056 GCAATATGACGCCACCCACGGAGCTGCA-----GGACCAGACTTACTGACTG 6106

Qy 1946 aArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966

Db 6107 TCGGGAAGTCTGGGTGAGCCGACCGCACTCTGTGCCAATGACAGCTACATGTGTGGC 6166

Qy 1966 sNGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnS 1986

Db 6167 ATGGGAGCACTGCCGAGGGCCCTGGACACAGGGGCTGGGGCTCCCCAAGCTCAGT 6226

Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006

Db 6227 CAGGCTCCGTCTGTCCGTTCACTCCAGCCAGCAGATACCAGCTACATCCTGCGAGCTTC 6286

Qy 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL 2026

Db 6287 CCAAAGATGACCTCATCTGTCTCAGCCCCACAGCGCCCAACCTGGGGCACCATCCCCA 6346

Qy 2026 ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046

Db 6347 AACTGCCCCACAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGAGCAA 6406

Qy 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV 2066

Db 6407 TAAGGACTGACTCCTTGACGTTCAAGGTCTGGGCAGCCGGGAAGACCTGCTGGCAGAGG 6466

Qy 2066 alSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleG 2086

Db 6467 TGAGTGGGCCCTCCCCGCCCTTGGCCGGGCCTACTCTTTCTGGGGCCAGTCAAGTACCC 6526

Qy 2086 lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlap 2106

Db 6527 AGGCACAGCAGCACTCCCGCAGCCAGCAAGATCTCCAAGCACATGACCCCGCCAGCCC 6586

Qy 2106 roCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSerLeuG 2126

Db 6587 CTTGCCCAGGCCCCAGAACCCCACTGGGGCAAGGGCCCTCCAGAGACCAGAAAGCACTTAG 6646

Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluG 2145

Db 6647 AGTTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTGCCCCCTGGCGGCCAGGAGG 6706

Qy 2145 luProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgA 2165

Db 6707 AGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGGCCAGAGCTGCCAGC 6766

Qy 2165 rgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA 2185

Db 6767 GCCGGCCTACGCTCGCTGGATGACAGAGGAGACACTCTATCGCCGTAGCTGCCTGG 6826

Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG 2205

Db 6827 ACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTG 6886

Qy 2205 lyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProp 2225

Db 6887 GGGGGCCTGGGAGCCGGCCCCCAAGAAAAAACAATCAGCCCGCCTAGTATCACCATAGACCCCC 6946

Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlap 2245

Db 6947 CCGAGAGCCCAAGGTCCTCGGACCCCGCCCGCCCTGGTATCTGCCTCCGGAGGAGGGCTC 7006

Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265

Db 7007 CGTCCAGCGCACTCCAAGGATCCCTTGGCCTCTGGCCCCCCTGACAGCATGGCTGCCTCGC 7066

Qy 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMeta 2285

Db 7067 CCTCCCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCTCTTGACCCAGCAGACCTGG 7126

Qy 2285 spPro 2286

Db 7127 ACCCC 7131

RESULT 5

US-10-757-262-15

; Sequence 15, Application US/10757262

; Publication No. US20040197825A1

; GENERAL INFORMATION:

; APPLICANT: Karicheti, Venkateswarlu

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Eliasof, Scott D.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,

; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,

; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,

; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,

; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,

; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,

; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,

; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

; TITLE OF INVENTION: 55053

; FILE REFERENCE: MF103-007P1RNOWNIM

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; PRIOR APPLICATION NUMBER: US 60/457,901

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; PRIOR APPLICATION NUMBER: US 60/468,775

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; PRIOR APPLICATION NUMBER: US 60/471,614

; PRIOR FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: US 60/478,742

; PRIOR FILING DATE: 2003-06-16

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; PRIOR FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: US 60/491,156

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; PRIOR APPLICATION NUMBER: US 60/499,594

; PRIOR FILING DATE: 2003-09-02

; PRIOR APPLICATION NUMBER: US 60/506,332

; PRIOR FILING DATE: 2003-09-26

; NUMBER OF SEQ ID NOS: 136

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 7648

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1) ... (7134)

US-10-757-262-15

Alignment Scores:

Pred. No.: 0 Length: 7648

Score: 10845.50 Matches: 2105

Percent Similarity: 89.72% Conservative: 33

Best local Similarity: 88.33% Mismatches: 110

Query Match: 90.17% Indels: 135

DB: 18 Gaps: 7

US-09-611-257A-24 (1-2287) x US-10-757-262-15 (1-7648)

Qy 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53

Db 2 TGGACGAGGAGGAGGATGGAGCGGCGCCGAGGAGTCGGACAGCCCCCGAGGCTTCATGC 61

Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73

Db 62 GGCTCAACGACCTGTCGGGGCCGGGGCCGGGGCCGGGGTCAGCAGAAAAGGACC 121

Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93

Db 122 CGGCAGCGCGGACTCGAGCGGAGGGGCTGCCGTACCCGGCGTGGCCCCCGGTGTT 181

Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCCTTACTTGAGCCAGACAGCCCGCGGAGCTGGTGCTCCGACCGTCTGTAACC 241

Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CCTGGTTGAGCGCATCAGCATGTTGGTCATCCTTCTCAACTGCGTGACCTGGGCATGT 301

Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153

Db 302 TCCGGCCATCGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCCTTG 361

Qy 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGAAGATGGTGGCCTTGGGCA 421

Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193

Db 422 TCCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481

Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213

Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACTGTCAGCTTCTCAGCTGTCAAG 541

Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATCGCATCCTTG 601

Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253

Db 602 TCACGTTGCTGCTGGATACGCTGCCCATGCTGGGCAACGTCTCTGCTGCTTCTTCG 661

Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273

Db 662 TCCTTCATCTTCGGCATCTGCGCGTCCAGCTGTGGCAGGGCTGTTCGGAACCGAT 721

Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293

Db 722 GCTTCCTACCTGAGAAATTTACGCTCCCTTGAGCGTGGACCTGGAGCGGTATTACCAGA 781

Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313

Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGTCTCCAGCCACGCGAGAACGGCATGCGGT 841

Qy 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333

Db 842 CCTGCAGAAAGCGTGCCACGCTGCGGGGACGCGGGCGGTGGCCCCACCTTGCGGTCTGG 901

Qy 333 spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353

Db 902 ACTATGAGGCTTACAACAGCTCCAGCAACACCCTGTGTCAACTGGAACCACTACTACA 961

Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373

Db 962 CCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCATCAACTTTGACAAACATTG 1021

Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393

Db 1022 GCTATGCTGATCGCCATCTTCCAGTTCATCAGCTGGAGGGCTGGTCCGACATCATGT 1081

Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413

Db 1082 ACTTTGTGATGGATGCTCATTCCTTCTACAATTTCACTTCACTTCTCTCTCATCATCG 1141

Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT 433

Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGAATTGCCACGCAGTTTCTCAGAGA 1201

Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453

Db 1202 CCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGGTTGTGCGGTTCTCTGTCCAACGCCA 1261

Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473

Db 1262 GCACCCCTGGCTAGCTTCTCTGAGCCCGGACGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321

Qy 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493

Db 1322 TGTACATCCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381

Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513

Db 1382 GGGTTGGGCTGCTCAGCAGCCACGACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441

Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533

Db 1442 GCTGCTCTCGTCTCCACCGCCCGCTATCCGTCCACCACTGGTGCCACCACCACCACC 1501

Qy 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553

Db 1502 ATCACCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGA 1561

Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573

Db 1562 TCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGTGCCACCACTTCGACGCGCTG 1621

Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681

Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613

Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGTCCCCTCTGAGGCATCCG 1741

Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633

Db 1742 GCAGGACTGTGGCAGCGGGAAGTGTATCCACCGTGCACACGAGCTCCACCTCCACCGGAGA 1801

Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653

Db 1802 CGCTGAAGGAGAAGGCACTAGTAGGTGGCTGCCAGCTCTGGCCCCCAACCTTCACCA 1861

Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673

Db 1862 GCCTCAACATCCCAACCCGGGGCCCTACAGTCCATGCACAAGTGTCTGGAGACACAGAGTA 1921

Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693

Db 1922 CAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGTCTGAAAAGCAGACAGTGGAG 1981

Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713

Db 1982 CCTGTGTTCCAGACAGTGCCTTACTGTGCCCGGGCCGGGGCAGGGAGGTGGAGCTCG 2041

Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733

Db 2042 CCGACCGTGAAATGCCTGACTCAGACAGCAGGCGAGTTTATGAGTTCACACAGGATGCC 2101

Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753

Db 2102 AGCACAGCGACCTCCGGGACCCCCACAGC--CGGGCGCAACGGAGCTGGGCCCAGATG 2158

Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773

Db 2159 CAGAGCCCAGCTCTGTGTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218

Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793

Db 2219 TGGACAGCAAGTACTTTTGGCCCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCA 2278

QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCACGAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
QY 813 leValPheThrSerLeuPheAlaIleuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTCACCAGCCTCTTTGGCCTGGAGATGCTGCTGAAGCTGCTTGATGGTCCCT 2398
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2399 TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTCTATTGTTGTCATCAGCGTGT 2458
QY 853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGCGGCCTGTTCGGTGTCTGGGACCTTCGCCCTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGGTGGCTTCCTGCGCGCTGCAGCGGCAGCTGGTGGTGTCTCATGA 2578
QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCATGGACAACGTGGCCACCTTCTGCATGCTGCTATGCTCTTTCATCTTCATCTTCA 2638
QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCC 2698
QY 933 euProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGAAATTTTGACTCTTGCTCTGGGCCATGCTCACTGCTTTTCAGATCC 2758
QY 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
Db 2759 TGACCCAGGAGACTGGAACAAAGTCCTCTACAATGGTATGGCCTCCACGTCCTCTGGG 2818
QY 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTTATTTCATTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGG 2878
QY 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TCGCCATTCTGGTGGAGGCTTCAGCGGAGGAAATCAGCAAAACGGGAAGATGCGAGTG 2938
QY 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTTAAGCTGTATTACGCTGCCTGTGCACTCCCAGGGGGAGATGCCAACAAAGTCCG 2998
QY 1010 luSerGluProAspphePheSerProSerValAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTGGGACAGGAAGAAAGTGCT 3058
QY 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI 1050
Db 3059 TGGCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGTGCGCCCTCTCA 3118
QY 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACACGGCCGCCACACCCATGTGCTGCCCCAAGACACACGACCGGGCCTGGGCG 3178
QY 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGCGCTGGGCCCTGCGTTCGGCCCGCACCCAGCAGCAGCGGGTGGCAGAGCCCTGGGGCGG 3238
QY 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA 1110
Db 3239 CC---CACGAGATGAAGTCAACGCCAGCGCCCGCAGCTCTCCGCACAGCCCCCTGGAGCG 3295
QY 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3296 CTGCAAGCAGCTGGACCGAGCGGCTCCAGCCGGAAACGCTTCGGCCGTGCACCCAGCC 3355
QY 1130 euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluS 1150

Db 3356 TGAAGCGGAGAAAGCCCAAGTGGAGAGCGCGGTCCCTGTTGTTCGGAGAAAGCCAGGAGA 3415
QY 1150 erGlnAspGluGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGGATGAAGAGGAGAGCTCAGAAGAGGAGCGCGCCAGCCCTGCGGGCAGTGACCATC 3475
QY 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCCTTTGACCTGCCACACACTGC 3535
QY 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3536 AGGTGCCAGGGTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACAGGACT 3595
QY 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCAATGGCAAGTCGGCTTCAGGGCGCCTGGCCCGGGCCCTGCGGCCTGATGACCCCCAC 3655
QY 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250
Db 3656 TGGATGGGATGACCGCGATGACGAGGGCAACCTGAGCAAAGGGAAACGGGTCCGCGCGT 3715
QY 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
Db 3716 GGATCCGAGCCCCGACTCCCTGCCTGTGCTCGAGCGAGACTCCTGGTCAAGCTACATCT 3775
QY 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3776 TCCCTCCTCAGTCCAGGTTCCGCTCCTGTGTACCGGATCATCCCCACAAGATGTTTCG 3835
QY 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
Db 3836 ACCAGTGGTCTTGTTCATCATCTTCTTAACGTGCATCACCATCGCCATGGAGCGCCCA 3895
QY 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
Db 3896 AAATTGACCCCCACAGCGCTGAACGCATCTTCTGACCTCTCCAATTACATCTTCACCG 3955
QY 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluG 1350
Db 3956 CAGTCTTTCTGGCTGAATGACAGTGAAAGTGGTGGCACTGGGCTGGTGTCTCGGGGAGC 4015
QY 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
Db 4016 AGCGTACCTGCGGAGCAGTTGGAACGTGCTGGACCGGCTGTTGGTGTCTCATCTCCGTCA 4075
QY 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
Db 4076 TCGACATTCTGGTGTCCATGCTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGG 4135
QY 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4136 TGCTCGGCTGTCTCGGACCTCGCCCGCTCAGGCTGATCAGCCGGCGCAGGGGCTGA 4195
QY 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
Db 4196 AGCTGGTGGTGAGACGCTGATGTCTCACTGAACCCCATCGGCAACATTGTAGTCATCT 4255
QY 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
Db 4256 GCTGTGCCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTT 4315
QY 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
Db 4316 TCGTGTGCCAGGGCGAGGATACAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCA 4375
QY 1470 erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4376 GTTACCGTGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCC 4435
QY 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlav 1510

Db	4436	TGTTTCGTTTGGCCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTG	4495
QY	1510	alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIles	1530
Db	4496	TGGGCGTGGACGAGCCCATCATGAACACACACCCCTGGATGCTGCTGACTTTCATCT	4555
QY	1530	erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluA	1550
Db	4556	CGTTCTCTGCTCATTTGGCCCTTCTTTGTCCTGAACATGTTTGTGGTGTGGTGGAGA	4615
QY	1550	snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysA	1570
Db	4616	ACTTCCACAAGTGTGGCAGCACAGAGGAAGAGGAGGCCCGCGGGGAGGAGAAC	4675
QY	1570	rgLeuArgArgLeuGluLysLysArgArg	1579
Db	4676	GCCTACGAAGACTGGAGAAAAAGAGAAGGAATCTAATGCTGGACGATGTAATTGCTTCCG	4735
QY	1580	--SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA	1599
Db	4736	GCAGCTCAGCCAGCGCTCGCTCAGAAGCCCACTGCAACCTTACTACTCCGACTACTCCC	4795
QY	1599	rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG	1619
Db	4796	GCTTCGGGCTCCTCGTCCACCACCTTGTGCAACGACCTACTCTGGACCTCTTCATCACAG	4855
QY	1619	lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL	1639
Db	4856	GTGTCATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCAGACGCCAGATTCTC	4915
QY	1639	euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV	1659
Db	4916	TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTCATCTTTGTCTTGGAGTCTCAG	4975
QY	1659	alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA	1679
Db	4976	TTTTCAAACCTTGTGGCCTTTGGTTTCCGTCCGTTCTTCCAGGACAGGTGGAACCCAGCTGG	5035
QY	1679	spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL	1699
Db	5036	ACCTGGCCATTGTGCTGTCTCCATCATTGGGCATCACGCTGGAGGAAATCGAGTCAACG	5095
QY	1699	euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV	1719
Db	5096	CCTCGCTGCCCCATCAACCCCAACCATCATCCGCATCATGAGGTGCTGCGCATTGCCCGAG	5155
QY	1719	alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA	1739
Db	5156	TGCTGAAGCTGCTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACGGTGTATGCAGG	5215
QY	1739	laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759
Db	5216	CCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTTTCTTTCATCTTTGCAG	5275
QY	1759	laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL	1779
Db	5276	CTCTGGCGTGGAGCTCTTTGGAGACCTTGAGTGTGACAGACACACCCCTGTGAGGGCC	5335
QY	1779	euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals	1799
Db	5336	TGGGCGTCTATGCCACCTTTCGGAACCTTTGGCATGGCCCTCTCTAACCTCTTCCGAGTCT	5395
QY	1799	erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS	1819
Db	5396	CCACAGGTGACAAATTGGAATGGCATTTATGAAGGACACCCCTCCGGGACTGTGACCCAGGAGT	5455
QY	1819	erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG	1839
Db	5456	CCACCTGCTACAAACACGGTCACTCGCCCTATCTACTTTTGTCTCTTCTGCTGACGGCCC	5515
QY	1839	inPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL	1859
Db	5516	AGTTCTGTCTAGTCAACCGTGGTGTATCGCGTGTGTATGAAGACCTGGAGGAGAGCAACA	5575

QY	1859	ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuS	1879
DB	5576	AGGAGGCCAAGGAGGAGCCGAGCTAGAGGCTGAGCTGGAGCTGAAGACCCCTCA	5635
QY	1879	erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVala	1899
DB	5636	GCCCCCAGCCCACTCGCCACTGGGCAGCCCTTCTCTGGCCTGGGGTCGAGGGCCCCG	5695
QY	1899	snSerThrAspSerProLysProGlyAlaProHisThrAlaHisIleGlyAlaAlaS	1919
DB	5696	ACAGCCCCAGACAGCCCAAGCCTGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCCT	5755
QY	1919	erGlyPheSerLeuGluHisProThr	1927
DB	5756	CCCACCTTTTCCCTGGAGCACCCACGACAGGCAGGCTGTTTGACACCATATCCCTGCTGA	5815
QY	1927	-----	1927
DB	5816	TCCAGGGCTCCCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCCAGGGGGCC	5875
QY	1927	-----	1927
DB	5876	AGCCCTCTGCCTTCCCTTCTGTGCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAG	5935
QY	1927	-----	1927
DB	5936	CTGAGATGGAGSCTCTGTCTCTGACGTACAGAGATTGTGTCTGAACCGTCTCTGTCTCTAG	5995
QY	1927	-----	1927
DB	5996	CTCTACGGATGACTCTTTGCCTGATGACATGCACACACTCTTACTTAGTGCCTGGAGA	6055
QY	1928	----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV	1946
DB	6056	GCAATATGCAGCCCCACCCACGAGCTGCCA-----GGACCAGACTTACTGACTG	6106
QY	1946	alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA	1966
DB	6107	TGCGGAAGTCTGGGGTCAGCCGAACGCACTCTCTGCCAATGACAGCTACATGTGTGGC	6166
QY	1966	snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnS	1986
DB	6167	ATGGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCTGGGGGTCCCCAAAGCTCAGT	6226
QY	1986	erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP	2006
DB	6227	CAGGCTCCGTCTGTTCGTTCACTCCAGCCAGCAGATACCAGCTACATCCTGCAGCTTC	6286
QY	2006	roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL	2026
DB	6287	CCAAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCA	6346
QY	2026	ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaI	2046
DB	6347	AACTGCCCCCAACAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCAGCAGCAA	6406
QY	2046	leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV	2066
DB	6407	TAAGGACTGACTCCTTGACGTTTCAGGGTCTGGGTCAGCGGAGACCTGTGGCAGAGG	6466
QY	2066	alSerGlyProSerCysProLeuThrArgSerSerSerPheTipGlyGlySerSerIleG	2086
DB	6467	TGAGTGGGGCCCTCCCCCGCCCTGGCCCGGCTACTCTTTCTGGGGCCAGTCAAGTACCC	6526
QY	2086	lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaP	2106
DB	6527	AGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCC	6586
QY	2106	roCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuG	2126
DB	6587	CTTGCCCGAGGCCCCAGAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAGCAGCTTAG	6646

Qy	2126	luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluG	2145
Db	6647	AGTTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTGCCCCCTGGCGGCAGGAGG	6706
Qy	2145	luProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgA	2165
Db	6707	AGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGCCACAGAGCTGCCAGC	6766
Qy	2165	rgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA	2185
Db	6767	GCCGGCCTACGTCTCGCTGGATGAGCAGAGGAGACACTCTATCGCCGTCAGCTGCCTGG	6826
Qy	2185	spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG	2205
Db	6827	ACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTAACTTGGGGCCAGCCTCTTG	6886
Qy	2205	lyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProp	2225
Db	6887	GGGGGCTGGAGCCGGCCCCAAGAAAACTCAGCCCGCCTAGTATCACCATAGACCCCC	6946
Qy	2225	roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaAp	2245
Db	6947	CCGAGAGCCAAAGTCTCGGACCCCGCCAGCCCTGGTATCTGCCTCCGGAGGAGGGCTC	7006
Qy	2245	roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP	2265
Db	7007	CGTCCAGGACTCCAAGGATCCCTTGGCCTCTGGCCCCCTTGACAGCATGGCTGCCTCGC	7066
Qy	2265	roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA	2285
Db	7067	CCTCCCCAAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCCTCTGACCCACGACACCTGG	7126
Qy	2285	spPro	2286
Db	7127	ACCC	7131

RESULT 6

US-10-062-674-2011
; Sequence 2011, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
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; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2011
; LENGTH: 8116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 404183.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (8116)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-2011

Alignment Scores:	
Pred. No.:	0
Score:	10707.00
Percent Similarity:	89.92%
Best Local Similarity:	87.75%
Query Match:	89.02%
DB:	17
Length:	8116
Matches:	2098
Conservative:	52
Mismatches:	130
Indels:	112
Gaps:	6
US-09-611-257A-24 (1-2287) x US-10-062-674-2011 (1-8116)	

Db	1401	CTTTCAAGGGGCCATCAACTTTTGACAACTTGGCTATGGCTATGCCTGGATGCCCATCTTCCAGG	1460
Qy	382	alileThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	1461	TCATACGCTGGAGGGCTGGGTGACATCATGTACTTTGTGATGGATGCTCATTTCTTCT	1520
Qy	402	yrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuC	422
Db	1521	ACAAATTCATCTACTTTCATCCTCCTCATCATCGTGGCTCCTTCTTCATGATCAACCTGT	1580
Qy	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMeta	442
Db	1581	GCCTGGTGGTGTATGCCACGCAGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATGC	1640
Qy	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1641	GGGAGCAGCGTGTGCGGTTCCTGTCCAAACGCAGCACCTTGGCTAGCTTCTCTGAGCCCG	1700
Qy	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
Db	1701	GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTACATCCTTCGTAAAGGCAGCCCGCA	1760
Qy	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1761	GGCTGGCTCAGGTCCTCGGGCAGCAGGTGCGGGTTGGCTGCTCAGCAGCCAGCAC	1820
Qy	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1821	CCCTCGGGGCCAGGAGACCCAGCCCCAGCAGCTGCTCTCGCTCCACCGCCGCTAT	1880
Qy	522	erValHisHisLeuValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnG	542
Db	1881	CCGTCCACCACCTGGTGNNNNNNNNNNNNNNNNNNNNNNNNTACCACTGGGCAATG	1940
Qy	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySera	562
Db	1941	GGACGCTCAGGGCCCCCGGGCCAGCCCCGAGATCCAGGACAGGGATGCCAATGGGTCCC	2000
Qy	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	2001	GCCGGCTCATGTGCCCCACCACCTCGACGCCTGCCCTCTCCGGGGCCCCCCTGGTGGCG	2060
Qy	582	laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2061	CAGAGTCTGTGCACAGCTTACCATGCCAGTCCGACTGACCTAGAGCCAGTCCGCTGCCAGG	2120
Qy	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2121	CGCCCCCTCCCAGGTCCCCCATCTGAGGCATCCGGCAGGACTGTGGGCAGCGGGAAGGTGT	2180
Qy	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2181	ATCCCAACCGTGCACACCAGCCCTCCACCGAGACCGCTGAAGGAGAAGGCACCTAGTAGAGG	2240
Qy	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2241	TGGTGTCAGCTCTGGGCCCCCAACCTCACCAGCCTCAACATCCCCACCGGGGCCCTACA	2300
Qy	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2301	GCTCCATGCACAAGCTGTGGAGACACAGAGTACAGGTGCTGCCAAAGCTCTTGCAAGA	2360
Qy	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2361	TCTCCAGCCCTTGCTTGAAGCAGACAGTGGAGCCTGTGGTCCAGACAGCTGCCCTACT	2420
Qy	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2421	GTGCCCCGGSCGGGCAGGGGAGGTGGAGCTCGCCGACCGGTGAAATGCCTGACTCAGACA	2480
Qy	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742

QY	1102	erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA	1122
Db	3616	GCTCTCCGCACAGCCCTGGAGCGCTGCAAGCAGCTGGACCAGAGCGCTCCAGCCGGA	3675
QY	1122	snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL	1142
Db	3676	ACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGAGAAGCCCAAGTGGAGAGCGCGGTCCC	3735
QY	1142	euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAspArgA	1162
Db	3736	TGTTGTCCGGAGAAAGCCAGGAGAGCCAGGATGAAGAGAGAGACTCAGAAGAGAGCGGG	3795
QY	1162	laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluAlaLysSerS	1182
Db	3796	CCAGCCCTCGGGCAGTAGCCATCGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGATT	3855
QY	1182	erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS	1202
Db	3856	CCTTTGACCTGCCAGACACACTGCAGGTGCCAGGCTGCATCGCACTGCCAGTGGCCGAG	3915
QY	1202	erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT	1222
Db	3916	GGTCTGCTTCTGAGCACAGGACTGCAATGGCAAGTCGGCTTCAGGGCGCCTGSGCCGGG	3975
QY	1222	hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsnLeuS	1242
Db	3976	CCCTGCGGCCTGATGACCCCCCACTGGATGGGGATGACCCGATGACGAGGGCAACCTGA	4035
QY	1242	erLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGluA	1262
Db	4036	GCAAGGGGAACGGGTCCGGCGGTGGATCCGAGGCCGACTCCCTGCCTGCTGCCTCGAGC	4095
QY	1262	rgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCysHisA	1282
Db	4096	GAGACTCCTGGTCAGCCTACATCTTCCCTCCTCAGTCCAGGTTCCGCCTCCTGTGTCAAC	4155
QY	1282	rgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI	1302
Db	4156	GGATCATCACCCACAAGATGTTGCACACCGTGGTCTTGTTCATCATCTTCTTAACTGCA	4215
QY	1302	leThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuT	1322
Db	4216	TCACCATCGCCATGGAGCGCCCCAAAATTGACCCCCACAGCGCTGAACGCATCTTCTCTGA	4275
QY	1322	hrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValA	1342
Db	4276	CCCTCTCCAATTACATCTTCACCGCAGTCTTTCTGGCTGAAATGACAGTGAAGTGGTGG	4335
QY	1342	laLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspG	1362
Db	4336	CAC TGGGCTGGTCTTCGGGGAGCAGGCGTACCTGCGGAGCAGTTGGAACGTCGTGGACG	4395
QY	1362	lyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyT	1382
Db	4396	GGCTGTTGGTGCTCATCTCCGTCAATCGACATTTCTGGTGTCATGGTCTCTGACAGCGGCA	4455
QY	1382	hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgV	1402
Db	4456	CCAAGATCCTGGGCATGCTGAGGGTGCTGCGGCTGCTGCGGACCCCTGCGCCCGCTCAGGG	4515
QY	1402	alIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysP	1422
Db	4516	TGATCAGCCGGCGCAGGGGCTGAAGCTGGTGGTGGAGACGCTGATGTCTCTCACTGAAAC	4575
QY	1422	roIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyV	1442
Db	4576	CCATCGGCAACATTGTAGTCATCTGCTGTGCTCTTCTCATCATTTTCGGGCATCTTGGGGG	4635
QY	1442	alGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrA	1462
Db	4636	TGCAGCTCTTCAAAGGGAAGTTTTCGTGTGCCAGGCGGAGGATACCGAGGACATCACCA	4695

QY	1462	snLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsn	PheAspA	1482
DB	4696	ATAAATCGGACTGTGCGAGGCCAGTTACCGGTGGTCCGGCACAAGTACAACATTGACA	4755	
QY	1482	snLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrValAspI	1502	
DB	4756	ACCTTGGCCAGGCCCTGATGCTCCCTGTTTCGTTTGGCCCTCAAGGATGGTGGGTGGACA	4815	
QY	1502	leMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsn	1522	
DB	4816	TCATGTACGATGGGCTGGATGCTGTGGGGCTGGACGACGACCCCATCATGAACCAACACC	4875	
QY	1522	roTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPheValLeuAsn	1542	
DB	4876	CCTGGATGCTGCTGTACTTTCATCTCGTTCCTGCTCATTTGTGGCCCTTCTTGTCTGAACA	4935	
QY	1542	etPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGlu	1562	
DB	4936	TGTTTGTGGTGTGGTGGAGAACTTCCACAAGTGTGGCAGCACCCAGGAGGAAGAGG	4995	
QY	1562	luAlaArgArgArgGlu-GluLysArgLeuArgLeuGluLysLysArgArgSerLys	1581	
DB	4996	AGGCCCGCGGGAGGAGCGCCCTACGAAGACTGGCGAAAGAGACGACGACGTAG	5055	
QY	1582	GluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArg	1601	
DB	5056	GAGAAGCAGATGGCTGAAGCCAGTGCAACCTTACTTCCGACTACTCCCGCTTCCGG	5115	
QY	1602	LeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIle	1621	
DB	5116	CTCCTCGTCCACCACCTTGTGCACCCAGCCACTACCTGGACCTCTTTCATCACAGGTGTATC	5175	
QY	1622	GlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGlu	1641	
DB	5176	GGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACGACGACCCAGATTCTGGATGAG	5235	
QY	1642	AlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLys	1661	
DB	5236	GCTCTGAAGATCTGCACTTACATCTTCACTGTCTTGTCTTGGAGTCAGTTTTCAAA	5295	
QY	1662	LeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAla	1681	
DB	5296	CTTGTGGCCTTTGGTTTCGTGGTCTTCCAGSACAGGTGGAAACCAGCTGGACCTGGCC	5355	
QY	1682	IleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeu	1701	
DB	5356	ATTGTGCTGCTGCCATCATGGGCATCACGCTGGAGGAAATCGAGGTCAACGCCTCGCTG	5415	
QY	1702	ProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLys	1721	
DB	5416	CCCATCAACCCACCACCATCATCCGCATCATGAGGTGCTGCGCATTGCCCGAGTGTGAAG	5475	
QY	1722	LeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuPro	1741	
DB	5476	CTGCTGAAGATGGCTGTGGCATGCGGGCGTCTGGACACGGTGTATGAGGCCCTGGCC	5535	
QY	1742	GlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGly	1761	
DB	5536	CAGGTGGGGAACCTGGGACTTCTTTCATGTTGTGTTTTTTCATCTTTTGCAGCTCTGGGC	5595	
QY	1762	ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg	1781	
DB	5596	GTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCTTGGGCCGT	5655	
QY	1782	HisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGly	1801	
DB	5656	CATGCCACCTTTTCGGAACCTTGGCATGGCCCTTCCCTAACCTCTTCCGAGTCTCCACAGGT	5715	
QY	1802	AspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGlnGluSerThr	1820	
DB	5716	GACAAATTGGAATGGCAATTATGAAGGACACCCCTCCGGGACTGCACCCACGACGAGCGCAGC	5775	
QY	1821	CysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheValLeuThrAla	1838	

Query Match:	50.74%	Indels:	4
DB:	19	Gaps:	2
US-09-611-257A-24 (1-2287) x US-10-930-301-51 (1-3993)			
QY	3	ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer	22
Db	281	CGCCGGGGCCCCCGGTTGCGTGAGGACACCTCCTCTGAGGGGCGCCCTTGCCTCT	340
QY	23	SerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgArgMetGluArgAla	42
Db	341	CGGATCGCCCGGGCCCCCGCTGGCCAGAGGATGGACGAGGAGGATGGAGCGGGCG	400
QY	43	ProArgSerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGly	62
Db	401	CCGAGGAGTCGGGACAGCCCCGGAGCTTCATCGCGCTCAACGACCTGTGCGGGGCGGGG	460
QY	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG	82
Db	461	GCCGGCCGGGGCCGGGTTCAGCAGAAAAGGACCCGGGCAGCGCGACTCCGAGCGGAGG	520
QY	82	lyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgp	102
Db	521	GGCTGCCGTACCCGGCGCTGGCCCCGGTGTTTTCTTCTACTTGAGCCAGGACGCCGCC	580
QY	102	roArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValserMetLeuV	122
Db	581	CGCGGAGTGGTGTCTCCGCACGGTCTGTAAACCCCTGGTTTGAGCGCATCAGCATGTTGG	640
QY	122	alileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142
Db	641	TCATCCTTCTCAACTGCGTGACCTGGGCATGTTCCGGCATGCGAGGACATCGCCTGTG	700
QY	142	spSerGlnArgCysArgileLeuGlnAlaPheAspAspPheilePheAlaPheAlav	162
Db	701	ACTCCCAGCGCTGCCGATCCTGCAGGCCCTTGATGACTTCATCTTTGCCCTTCTTGGCG	760
QY	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA	182
Db	761	TGGAGATGGTGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAAAGTGTACCTGGGAG	820
QY	182	spThrTyrAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuA	202
Db	821	ACACTTGGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGGATGCTGGAGTACTCGCTGG	880
QY	202	spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
Db	881	ACCTGCAGAACGTGAGCTTCTCAGCTGTGAGACAGTCGCTGTGTCGACCGCTCAGGG	940
QY	222	laileAsnArgValProSerMetArgileLeuValThrLeuLeuLeuAspThrLeuProM	242
Db	941	CCATTAAACCGGTCGCCAGCATGCGCATCCTTGTACGTTGCTGTGATACGCTGCCCA	1000
QY	242	etLeuGlyAsnValLeuLeuLeuCysPheValPhePheIlePheGlyIleValGlyV	262
Db	1001	TGCTGGGCAACGTCTCTGCTCTGCTTCTTCGTCCTTCTTCATCTTCGGCATCGTCGGCG	1060
QY	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP	282
Db	1061	TCCAGCTGTGGCGAGGGCTGCTTCGGAAACCGATGCTTCCTACCTGAGAAATTCAGCCTCC	1120
QY	282	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPropheI	302
Db	1121	CCCTGAGCGTGGACCTGGAGCGCTATTACCAGACAGAGAACGAGGATGAGAGCCCTTCA	1180
QY	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	1181	TCTGTCTCCAGCCACCGAGAACGGCATGCGGTCTCTGAGAAAGCGTGGCCACGCTGCGCG	1240
QY	322	lyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSera	342
Db	1241	GGGACGGGGGGCGGTGGCCCCACCTTGGCGTCTGGACTATGAGGCGCTACAACAGCTCCAGCA	1300

QY	342	snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP	362
Db	1301	ACACCACCTGTGTCAACTGGAAACCACTACTACCAACTGCTCAGCGGGGAGCAAAACC	1360
QY	362	roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV	382
Db	1361	CCTTCAAGGGCGCCATCAACTTTGACAACATTGGCTATGCTTGATCGCCATCTTCCAGG	1420
QY	382	alileThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	1421	TCATCAGCTGGAGGGCTGGGTGCACATCATGTACTTTGTGTGATGGATGCTCAITCTTCT	1480
QY	402	yrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC	422
Db	1481	ACAATTCATCTACTTCATCTCTCTCATCATCGTGGGCTCCTTCTTCATGATCAACCTGT	1540
QY	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	1541	GCCTGGTGGTGATTGCCACGAGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATGC	1600
QY	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1601	GGGAGCAGCGTGTGCGGTTCTGTCCAACGCCAGCACCTGGCTAGCTTCTCTGAGCCCG	1660
QY	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
Db	1661	GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTAACATCTTCGTAAGGCAGCCGCA	1720
QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1721	GGCTGGCTCAGGTCTCTCGGCAGCAGGTGTGCGGGTTGGGCTGCTCAGCAGCCCGCAC	1780
QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1781	CCCTCGGGGGCCAGGAGACCCAGCCCGCAGCAGCTGCTCTCGTCCCACCGCGCTAT	1840
QY	522	erValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuGlyAsnG	542
Db	1841	CCGTCCACCACCTGGTGTACCAACACCACCATCACCACTACCACTGGGCAATG	1900
QY	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySera	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCCGAGATCCAGGACAGGATGCCAATGGGTCCC	1960
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGCTCATGTGTCACCAACCTCGACGCTGCCCTCTCCGGGGCCCCCTTGGTGGCG	2020
QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGCACAGCTTTCACATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2080
QY	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCCATCTGAGGCATCCGGCAGGACTGTGGCAGCGGGAAGGTGT	2140
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCACCGTGCACACCAAGCCTCCACCGAGACGCTGAAGGAGAGAGGACTAGTAGAGG	2200
QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyPropheS	662
Db	2201	TGGCTGCCAGCTCTGGGGCCCCAACCTTCACCAAGCTCAACATCCCACCCGGGCCCCACA	2260
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCATGCACAAGCTGCTGGAGACACAGAGTACAGGTGCCTGCCAAAGCTCTTGCAAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCAGCCCTTGTCTTGAAGCAGACAGTGGAGCCTGTGGTCCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722

Db 2381 GTGCCCCGGCCGGGAGGAGGTGGAGCTGCCGACCGTGAAATGCCTGACTCAGACA 2440
QY 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS 742
Db 2441 CGGAGGCAGTTTATGAGTTTACACAGGATGCCAGCAGCACGACGACCTCCGGGACCCCA 2500
QY 742 erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 2501 GC---CGGCGGCAACGAGCGCTGGGCCAGATGCAGAGCCAGCTCTGTGCTGGCCTTCT 2557
QY 762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 2558 GGAGGCTAATCTGTGACACCTTCCGAAAGATTGTGACAGCAAGTACTTTGGCCGGGAA 2617
QY 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db 2618 TCATGATCGCCATCCTTGTCAACACACTCAGCATGGGCATCGAATACACAGCAGCCCG 2677
QY 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db 2678 AGGAGCTTACCAACGCCCTTAGAATCAGCAACATCGTCTTACCAGCCTCTTTGCCCTGG 2737
QY 822 luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db 2738 AGATGCTGCTGAAGCTGCTTGTGTATGTTGCCCTTGGCTACATCAAGAATCCCTACA 2797
QY 842 lePheAspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyGlyG 862
Db 2798 TCTTCGATGGTGTCAATTGTTGTTATCAGCGTGTGGGAGATCGTGGGCCAGCGGGGGCG 2857
QY 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
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QY 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 2918 CGGCGCTGCAGCGGCAGCTGGTGTGCTCATGAAGACATGGACAACGTGGCCACCTTCT 2977
QY 902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 2978 GCATGCTGCTTATGCTCTTTCATCTTCATCTTTCAGCATCTTCCAGCATCTGGCATG 3037
QY 922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db 3038 GCAAGTTTGCCTCTGAGCGGATGGGACACCTCGCCAGACCGGAAAGATTTTGACTCCT 3097
QY 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962
Db 3098 TGCTCTGGGCCATCGTCACTGTCTTTTCAGATCTGATCCAGCCAGGAGCTGGAACAAGTCC 3157
QY 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
Db 3158 TCTACAAATGGTATGGCTCCACGTCGTCGCGGGCGGCTTTATTTTCATTGCCCTCATGA 3217
QY 982 hrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 3218 CTTTCGGCAACTACGTGCTCTTCAATTTGCTGTCGCCATTTCTGGTGGAGGGCTTCCAGG 3277
QY 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
Db 3278 CGGAGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTCTTCTCAGCCCTGGATG 3337
QY 1022 lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
Db 3338 GTGATGGGGACAGGAAGATGCTTGGCTTGGCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGC 3397
QY 1042 rgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062
Db 3398 GGAAGAGCCTGTGCGCGCTCTCATCATCCACAGGCGGCCACACCATGTCGTGCCCA 3457
QY 1062 ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers 1082

Db 3458 AGAGCACACGACGGGCTGGGCGAGGCGCTGGGCCCTGCGTCGCGCCGACACGACGACA 3517
QY 1082 erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
Db 3518 GCGGGTCGGCAGAGCTGGGGCGGCC---CACGAGATGAAGTACACGCCCCAGCGCCCGCA 3574
QY 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA 1122
Db 3575 GTCTCCGCACAGCCCTGGAGCGCTGCAAGCAGCTGGACCAGCAGGCGCTCCAGCCGGA 3634
QY 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142
Db 3635 ACAGCTCGGCCGTGCACCCAGCCTGAAGCGGAGAAGCCCAAGTGGAGAGCGGCGTCCC 3694
QY 1142 euLeuSerGlyGluGlyGlnGlnSerGlnAspGluGluSerSerGluGluAspArgA 1162
Db 3695 TGTTGTCGGGAGAGGCCAGGAGAGCCAGGATGAAGAGGAGCTCAGAAGAGGAGCGGG 3754
QY 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers 1182
Db 3755 CCAGCCCTCGGGCAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGATT 3814
QY 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
Db 3815 CCTTTGACTGCCAGACACACTGCAGGTGCCAGGCTGCATCGCACTGCCAGTGGCCGAG 3874
QY 1202 erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3875 GGTCGTCTTCTGAGCACCCAGGACTGCAATGGCAAGTCCGCTTCAGGGCGCTGGCCCCG 3934
QY 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeu 1241
Db 3935 CCCTGCGGCTGATGACCCCCCACTGGATGGGATGACGCCGATGACGAGGCAACCTG 3993

RESULT 8
US-10-377-139-8
; Sequence 8, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-8

Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5432.50 Matches: 1234
Percent Similarity: 62.21% Conservative: 241
Best Local Similarity: 52.05% Mismatches: 514
Query Match: 45.17% Indels: 387
Gaps: 62
DB:

US-09-611-257A-24 (1-2287) x US-10-377-139-8 (1-6990)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 16 TCCCCGCCCTCCTCATCTGCAGCAGCCCCAGCCGCTGAGCCAGGAGTACCACGAGCAG 75
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 76 CCCGGACCCCGG----- 87

QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
 Db 88 -----AGCCCCCATCTCCCGCCAGGCTGGAGGAGCTCTGGATGGAGCT----- 135
 QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
 Db 136 -----GATCCT-----CATGTCCCACAC 153
 QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
 Db 154 CCAGACCTGGCGCCTATTGCCTTCTTCTGCCTGCGACAGACCACAGCCCCCGGAACCTGG 213
 QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
 Db 214 TGCAACAAGATGGTGTGCAACCGTGGTTTGAATGTGTGAGCATGTGTGTGATCTCTGCTG 273
 QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
 Db 274 AACTGCGTGACACTTGGCATGTACCAGCCGTGCGACGACATGGACTGCTCTCCGACCGC 333
 QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
 Db 334 TGCAAGATCTGCAGGTCTTTGATGACTTTCATCTTATCTTCTTTGCCATGGAGATGGTG 393
 QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
 Db 394 CTCAAGATGGTGGCCCTGGGGAATTTTGGCAAGAAAGTGTACTCTCGGGGACACATGGAAAC 453
 QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
 Db 454 CGCCTGGATTCTTTCATCGTCATGGCAGGATGGTTCGAGTACTCTCCCTGGACCTCAGAAC 513
 QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
 Db 514 ATCAACCTGTTCAGCCATCCGCAACCGTGCCTGAGGCCCTCAAAGCCATCAACCGC 573
 QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
 Db 574 GTGCCAGATGCGGATCCTGGTGAACCTGTCTCTGGACACACTGCCCATGCTGGGGAAT 633
 QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
 Db 634 GTCCCTGTGCTCTGCTTCTTTGTCTTCTTTCATCTTTGGCATCATAGGTGTGCAGCTCTGG 693
 QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
 Db 694 GCGGGCCTGTGCGTAACCGCTGCTTCTTGAGGAGAACTTCAACATACAAGGGGATGTG 753
 QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPropheIleCysSerGln 305
 Db 754 GCCTTGCCCCCATACTACCAGCGGAGGAGATGATGAGATGCCCTTCATCTGCTCCCTG 813
 QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
 Db 814 TCGGGCGACAATGGGATAATGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 867
 QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
 Db 868 ---GGCCGTGAGTGTGCTGTCCAAGGACGACGTCTACGACTTTGGGGGGGGCGCCAG 924
 QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
 Db 925 GACCTCAATGCCAGCGGCCCTCTGTGTCAACTGGAACCGTACTACAATGTGTGCCGACG 984
 QY 358 GlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
 Db 985 GGCAGCGCCCAACCCCAAGGGTGCCATCAACTTTGACAACATCGGTTATGTGTGGATT 1044
 QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
 Db 1045 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGAT 1104

QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
 Db 1105 GCTCACTCCTTCTACAACTTCACTTCACTTCACTGCTTATCATAGTGGCTCCTTCTTC 1164
 QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
 Db 1165 ATGATCAACCTGTGCTCGTGTGTATAGCGACCGAGTTCTCGGAGACCAAGCAACGGGAG 1224
 QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
 Db 1225 CACCGGTGATGCTGGAGCAGCGCGCTACTGTGCC--TCCAGCACGTGGCCAGC 1281
 QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
 Db 1282 TACGCCGAGCCTGGCGACTGTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTGCGC 1341
 QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
 Db 1342 AAGGCCAAGCGCGCCCTGGGCTCTTACAGGCCCTGCAGAGCCGCGCCAGGCCCTG 1401
 QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
 Db 1402 ---GGCCCGAGGCCCGGCCCCCGCCAAACCTGGGCC-- 1437
 QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHis 533
 Db 1438 -----CACGCCAAGGAGCCCGCCGCACTACCATGGGAAGACTAAG 1476
 QY 534 -----HisHisHisTyrHisLeuGlyAsn-----GlyThrLeuArgValPro 547
 Db 1477 CGTCAGGGAGATGAAGGGAGACATCTCGGAAGCGCGCATTTGCCAGACTTTGCATGGCCT 1536
 QY 548 ArgAlaSerPro-GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPr 567
 Db 1537 ---GCCTCCCTGGAAATGATCACTCGGGAAGAGAGCTGTGCCCGCAACATA---GCCCC 1590
 QY 567 oProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa 585
 Db 1591 CTGGATGCGACGCCCCACACCTTGGTGCAGCCCATCCCGCCACGCGC----- 1636
 QY 585 lHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
 Db 1637 -----TGGCTTCGATCCC 1650
 QY 605 oArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa 625
 Db 1651 GCCAGTGCCCTTGTGTCAGCATGAGGACGCGCGCGCCCTCGGGCCTGG----- 1702
 QY 625 lHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSe 645
 Db 1703 -----GCAGCACCGACTCGGGCCAGGAGGGCTCGGGCT----- 1735
 QY 645 rProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHi 665
 Db 1736 -CCGGAGCTCCGCTGTGGCG----- 1756
 QY 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685
 Db 1757 -----AGGACGAGCGGATGGG----- 1774
 QY 685 oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh 705
 Db 1775 -----AC 1776
 QY 705 rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVa 725
 Db 1777 GGGCCCCGAGCAGCGAGG----- 1795
 QY 725 lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgAr 745
 Db 1796 -----ACGGAGCCTCCTCAGAACTGGGGAGGAGG-----ACGAGGAGGAG 1836
 QY 745 gGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuI 765

Db 1837 GAGCAGCGGATGGGGCGGTCTGGCTG-TGGGGGATGTG-----TGGCGGGAGAC 1886
Qy 765 eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl 785
Db 1887 GCGAGCCAAGCTGCGCGGCATCGTGGACAGCAAGTACTTCAACCGGGGCATCATGATGC 1946
Qy 785 aIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuTh 805
Db 1947 CATCTGGTCAACACCGTCAGCATGGGCATCGAGCACCAAGAGAGCGGAGGCTGAC 2006
Qy 805 rAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLe 825
Db 2007 CAACATCCTGGAGATTCGAATGTGTCTTCACCAGCATGTTTGGCCTGGAGATCCT 2066
Qy 825 uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl 845
Db 2067 GAAAGCTGGCTGCATTTGGGCTCTTCGACTACCTGCGTAACCCCTACAACATCTTCGACAG 2126
Qy 845 yValIleValIleSerValTyrGluIleValGlyGlnGlnGlyGlyLeuSerVa 865
Db 2127 CATCATTTGTCATCATCATCGCATCTGGAGATCTGGGGCAGCGGCGGCTGGCTGCGGT 2186
Qy 865 lLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGl 885
Db 2187 GCTGGGACCTTCCGGCTGCTGCGCGTGTGAAACTGGTGGCTTCATGCTGCCCTGCG 2246
Qy 885 nArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe 905
Db 2247 GCGCAGCTCGTGGTGTCTCATGAAGACCATGGACAACGTGGCCACCTTCTGCATGCTGT 2306
Qy 905 uMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAl 925
Db 2307 CATGCTCTTCATCTTCATCTTCAGCATCTTGGGATGCATATTTTGGCTGCAAGTTTCAG 2366
Qy 925 aSerGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr 944
Db 2367 CCTCCGACGGACACTGGAGACACGGTGCCCGCAGGAAGAACTTCGACTCCCTGCTGTG 2426
Qy 944 pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAs 964
Db 2427 GGCCATCGTCACGTGTTCCAGATCCTCACCCAGGAGACTGGAACTGCTTCTCTACAA 2486
Qy 964 nGlyMetAlaSerThrSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl 984
Db 2487 TGGCATGGCTCCACTTCTCCTGGGCTCCCTCTACTTTGTGCGCCTCATGACCTTCGG 2546
Qy 984 yAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGl 1004
Db 2547 CAACATATGTGCTCTTCAACCTGCTGGTGGCCATCTCTGGTGGAGGCTTCCAGGGGAGGG 2606
Qy 1004 yAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal----- 1020
Db 2607 TGACGCCCAATCGCTCCTACTCGGACGAGGACCAGAGCTCATCCAACATAGAAGATTGA 2666
Qy 1021 -----AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAl 1034
Db 2667 TAAGCTCAGGAAGGCTGGACAGCAGCGGAGATCCCAAG-----CTCTGCCCAATCCC 2720
Qy 1034 aLeuGlyGluHisAlaGluLeuArgLysSerLeuProLeuIleIleHisThr-- 1053
Db 2721 CATGACCCCAATGGGCACCTGGACCCCAAGTCTC-----CCACTGGGTGGGCACCTAGG 2774
Qy 1054 -----AlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGl 1070
Db 2775 TCCTGTGGGGCTGGGGACCTGGC-----CCCCGACTCTCACTGCAGCGGACCCCAT 2828
Qy 1070 uAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl 1090
Db 2829 GCTGGTGGCCCTGGGCTCCCGAAAGACAGTGTATGTCTCTA-----GGGAGGAT 2879
Qy 1090 aHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAl 1110

Db 2880 GAGCTATGACCAGCGCTCCCTGTCTCCAGCTCCCGAGCTCTACTACGGGCCATGGGGCCG 2939
Qy 1110 aAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLe 1130
Db 2940 CAGCGCGGCTGGGCCAGCGCTCGCTCCAGCTGGAAC-----AGCCT 2981
Qy 1130 uLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGl 1149
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Db 3042 CGCCCGGCTGCGAGGTTGCCCGGACGAGGGGCGCGCGGCGCGCACCCCTGCACAC 3101
Qy 1167 rAspHis-----ArgHisAr 1172
Db 3102 CCCACACGCCACACACATTTCATCAGGGGCCCATCTTGGCGCACCGCCACCGCACCG 3161
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Qy 1309 oLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheTh 1329
Db 3576 TCAGATCGAGCGCGCAGCACCGAACGCTCTTCTCACCGTGTCCAACATACATCTTCAC 3635
Qy 1329 rAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGl 1349
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Qy 1349 uGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVa 1369
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Qy 1389 gValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLe 1409
Db 3816 AGTCTTGGGCTCTCTGCGCACCTTACGCCCTCGCTGTGTGTGTGTGTGTGTGTGTGTGT 3875
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RESULT 9

US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
Gaps: 60
DB:

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)

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Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278

Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCCTGGAGGAGCCTTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTCTTCTGCTGCGACAGACCACCGCCCCCGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGCTGTTTGAATGTGTGAGCATGCTGGTGATCCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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Qy 166 VallysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAGTACTACCTCGGGGACACATGGAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
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Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
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Qy 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
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Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
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Db 945 GCCTTGCCCCCATACTACCGCCGAGGAGGATGATGAGATGCCCTTCTATCTGCTCCCTG 1004
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QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
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QY 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
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QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Dbb 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCCTCTACCAGGCCCTGCAG 1574
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Dbb 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537
Dbb 1578 ---CGGCGCAGGCCCTG----- 1592
QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
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QY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
Dbb 1602 -----GCCCGCGCCCGCAACCTGGGCC----- 1628
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QY 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Dbb 1686 -----ACGCCCCACACC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIlePro 657
Dbb 1698 ---CTGGTGCAG-----CCCATCCCCGCCACGCTGGCTTCC----- 1730
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Dbb 1731 -----GATCCGCGCAGCTGCCCTTGTCTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Dbb 1758 CATGAGGACGGCGCGCCCTCGGGCCTGGGCAGCACCCGACTCGGGCCAGGAGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Dbb 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCGGAGCAGGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Dbb 1854 -----GATGGGACGGGGCC-----CGGAGCAGCGAGGACGGAGCCTCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Dbb 1899 CTGGGGAAGGAGGAGGAGGAGGAGCAG-----GCGGATGGGGCG 1940
QY 757 SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp 774

Dbb 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGAGACGCGAGCCAAGCTGCGCGGATCGTGGAC 2000
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Dbb 2001 AGCAAGTACTTCAACCGGGGCGATCATGATGGCCATCTCTGGTCAACACCGTCAGCATGGGC 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
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QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPropheGly 834
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Dbb 2181 TACCTGCGTAACCCCTACAAATCTTCGACAGCATCATTTGCATCATCAGCATCTGGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
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Db 4470 CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACCTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCCGCGCTCATCCACTCCATGTGCACCGCAGCCACTACCTGGACATCTTCATCACC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db 4569 TTCATCATCTCGCTCAACGTGGTCACCATGTCCCTGGAGSACTACAATCAGCCACCGTCC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCACTATATATGTTCCACCATGTCTTGTGTGGAGGCT 4688
QY 1659 ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1678
Db 4689 GTGCTGAAGCTGGTGGCATTTGGTCTGAGCGGCTTCTTCAAGGACCGATGGAACCGCTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGTGCTACTGTCTAGTCATGGGCATCACCCCTGGAGGAGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 GCGGCCCTGCCCATCAATCCCACCATCATCCGCATCATGAGGGTCTTGGCATTTGCCCGA 4868
QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTGCTGAAGCTGTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACCGTGGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
Db 4929 GCTTTGCCCCAGGTGGCAACCTTGGGCTCTCTTTCATGTGCTCTTCTTCTCATATGCT 4988
QY 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
Db 4989 GCTCTCGGGTGGAGCTCTTTGGGAAGCTGTCTGCAACGACGAGAAACCCGTGCGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db 5049 ATGAGCCGGCATGCCACCTTCGAGAACTTCGGCATGGCCTTCCTTCACACTCTTCCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln 1817
Db 5109 TCCACGGGTGACAACTGGAACGGGATCATGAAGGACACCGCTCGGGGACTGCACCCACGAC 5168

QY	1818	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1833
DB	5169	GAGCGCAGCTGCCTGAGCAGCCTGCAGTTTGTGTGCGCGCTGTACTTCTGAGCTTCGTG	5228
QY	1836	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu	1855
DB	5229	CTCACCGCGCAGTTCTGTCTCATCAACGTTGTTGGTGTGTCTCATGAAGCAGCTGGAC	5288
QY	1856	GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMet	1875
DB	5289	GACAGCAACAAGGAGCGCAGGAGGACGCCGAGATGGATGCCGAGCTCGAGCTGGAGATG	5348
QY	1876	--LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly	1894
DB	5349	GCCCATGGCCTGGCCCTGGCCCGAGGCTGCCTACCGGCTCC-----	5390
QY	1895	ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHis	1914
DB	5391	-----CGGGCGCCCTTGTGCCGCGGCGCG---5414	5414
QY	1915	IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro-----	1930
DB	5415	---GGAGGGCGGGCGCGG---GGCGACACCGAGGGCGGCTTGTGCCGCGGCTGCTACTC	5470
QY	1931	-----HisProGluGluValProValPro	1938
DB	5471	GCCTGCCCAGGACTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTCCGGCTCCAT	5530
QY	1939	LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1958
DB	5531	CTTCCACCACTACTCTCGCTGCCCTGCCGGCTGCCAAGAGTGTC-----CCA	5575
QY	1959	AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly	1978
DB	5576	CGACAA-----GCAAGAGGTGCAGTGGCTGAGACGGA	5608
QY	1979	TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp	1998
DB	5609	GGCCTTCTCCCTGAACCTCAGACAGGTCTCTCGTCCATCTGTGGTGACGACCTGAGTCT	5668
QY	1999	ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuGlnProHisGlyAla	2018
DB	5669	CGAGGA-----CCCCACAGCCTG	5686
QY	2019	ProThrTrpGlyAlaIleProLys-----	2026
DB	5687	CCCACCTGG-----CCGCAAGGACAGCAAGGTGAGCTGGACCCACCTGAGCCCAT	5737
QY	2027	---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla	2045
DB	5738	GCGTGTGGAGACCTGGGCGAATGCTTCTTCCCTTGT-CCTCTACGGCCGCTCGCCGG	5796
QY	2046	IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu	2065
DB	5797	ATCCAGAGAACTTCTCTGT---GTGAGATGGAGGAGATCCCAT-----TCAACC	5841
QY	2066	ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIle	2085
DB	5842	CTGTCCGGTCTCGCTGAAACATGACA-----	5868
QY	2086	GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla	2105
DB	5869	-----GCAGTCAAGCACCCCAAGTCCCTTCT	5895
QY	2106	ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu	2125
DB	5896	CCC-----CGGATGCCTCCAGCC-----	5913
QY	2126	GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu	2145
DB	5914	-----CTCTCTGCTCCATGCCAGCCGAGTTCTTCCACCCCTG	5949
QY	2146	ProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys	2163

Db	5950	CAGTGTGTGCCAGCCAGAAAGGCCAGAAAGGCACTGGCACTGGAAACCCCTCCCAAGA	6009
Qy	2164	ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys	2183
Db	6010	TTGCGCTG-CAGGGCTCTCTGGGCATCT-----CTGCGGTCAACAAGGTTCAACTGT	6059
Qy	2184	Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu	2199
Db	6060	ACCCTCTCCGGCAGGCCACCGGAGCGACACGTGCTGGACGCCAGCCCGCAG-CTC	6118
Qy	2200	GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSer	2219
Db	6119	CGCGGCGAGCCTGCAGACCACGCTCGAGGACAGCCTGACCTGAGCGCAGCCCCCGCG	6178
Qy	2220	IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly	2237
Db	6179	-----TGCCCTGGGGCCGCCCTGCTGCCAGGACCCCGGCG	6217
Qy	2238	ValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro	2257
Db	6218	CGGCTGTCCCCCGCGCTCGCGCGCCTGAGCTGCGCGCGCGGCGCTCTTCAGCCT	6277
Qy	2258	LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu	2277
Db	6278	GCGGGGCTGCGGGCGCATCAGCGCAGCCACAGCAGCGGGGGCTCCACCAGCCCGGCTG	6337
RESULT 10			
US-10-425-800-1			
; Sequence 1, Application US/10425800			
; Publication No. US20030180886A1			
; GENERAL INFORMATION:			
; APPLICANT: Dietrich, Paul S.			
; APPLICANT: McGivern, Joseph G.			
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;			
; TITLE OF INVENTION: AND USES			
; FILE REFERENCE: R0043B-REG sequence listing			
; CURRENT APPLICATION NUMBER: US/10/425,800			
; CURRENT FILING DATE: 2003-04-29			
; PRIOR APPLICATION NUMBER: US/09/404,650			
; PRIOR FILING DATE: 1999-09-23			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 6816			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (192)..(6716)			
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Alignment Scores:			
Pred. No.: 0 Length: 6816			
Score: 5420.00 Matches: 1223			
Percent Similarity: 61.74% Conservative: 234			
Best Local Similarity: 51.82% Mismatches: 494			
Query Match: 45.06% Indels: 413			
DB: 16 Gaps: 60			
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Qy	12	ThrProProLeuArgGlySerAlaArgProSerSerAspPro-----	25
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Qy	26	ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer	45
Db	267	CCCCGACCCCG-----	278
Qy	46	ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly	65
Db	279	-----AGCCCCCATCTCTCCCGCCAGCGCTGAGGAGGAGCTCTTGATGGAGCT-----	326

QY	66	AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr	85	QY	418	MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu	437
Db	327	-----GATCCT-----	344	Db	1356	ATGATCAACCTGTGCCTCGTTGTTCATAGCGACCCAGTTC	1415
QY	86	ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTyr	105	QY	438	SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer	457
Db	345	CCAGACCTGGCGCCTATTGCCTTCTTCTGCTGCGACAGACCAACGCCCCCGGAAC	404	Db	1416	CACCGGCTGATGCTGGAGCAGCGCGCAGCGCTACCTGTCC--TCCAGCACGGTGGCCAGC	1472
QY	106	CysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuValIleLeuLeu	125	QY	458	PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg	477
Db	405	TGCATCAAGATGGTGTGCAACCCGTGTTGAATGTGTACAGCATGCTGGTATCCTGCTG	464	Db	1473	TACGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCCTCGCG	1532
QY	126	AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145	QY	478	LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	497
Db	465	AACTGCGTGACACTTGGCATGTACACGCCGTGCGACGACATGGACTGCCTGTCGACCGC	524	Db	1533	AAGGCCAAGCGC-----CGCGCCCTGGGCTCTACCCAGGCCCTGCAG	1574
QY	146	CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal	165	QY	498	SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer	517
Db	525	TGCAAGATCCTGCAGGTCTTTGATGACTTTCATCTTTATCTTCTTGGCATGGAGATGGTG	584	Db	1575	AGC-----	1577
QY	166	ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn	185	QY	518	HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyr	537
Db	585	CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAGTGCTACCTCGGGGACACATGGAAC	644	Db	1578	---CGCGCCAGGCCCTG-----	1592
QY	186	ArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn	205	QY	538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	557
Db	645	CGCCTGGATTTCTTCATCGTCATGCGAGGATGGTTCGAGTACTCCCTGGACCTTCAGAAC	704	Db	1593	-----GGCCCGGAG-----	1601
QY	206	ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg	225	QY	558	AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly	577
Db	705	ATCAACCTGTAGCCATCCGCAACCTGCGCGTCTGAGGCCCTCAAGCCATCAACCGC	764	Db	1602	-----GCCCGGCCCGCCAAACCTGGGCC-----	1628
QY	226	ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn	245	QY	578	ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
Db	765	GTGCCCATGTCGGATCCTGGTGAACCTGCTCCTGGACACACTGCCCATGCTGGGAAT	824	Db	1629	-----CACGCCAAG-----GAGCCC	1643
QY	246	ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp	265	QY	598	ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly	617
Db	825	GTCCTGCTGCTCTGCTTCTTGTCTTCTTCTTCTTGGCATCATAGGTGTGAGCTCTGG	884	Db	1644	CGGCATACCAGCTGTGCCCGCAACATAGCCCCCTGGATGCG-----	1685
QY	266	AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal	285	QY	618	SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys	637
Db	885	GCGGCTGCTGCTGCTAACCGTGTCTTCTGGAGGAGAACTTCAACATACAGGGGATGTG	944	Db	1686	-----ACGCCCCACACC-----	1697
QY	286	AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPropheIleCysSerGln	305	QY	638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	657
Db	945	GCCTTGCCCCATACTACCAGCGGAGGAGATGATGAGATGCCCTTCACTGCTCCTCTG	1004	Db	1698	---CTGGTGCAG-----CCCATCCCGCCACGCTGGCTTCC-----	1730
QY	306	ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly	325	QY	658	ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys---	676
Db	1005	TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG-----	1058	Db	1731	-----GATCCCGCCAGCTGCCCTGTGCTGCCAG	1757
QY	326	GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer	339	QY	677	HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	696
Db	1059	---GGCCGTGAGTGTGCTGTCTCAAGGACGACCTTACGACTTTGGGCGGGCGCCAG	1115	Db	1758	CATGAGGACGGCGCGGCCCTCGGGCTGGGCGAGCACCGACTCGGGCCAGGAGGCTCG	1817
QY	340	SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrThrAsnCysSerAla	357	QY	697	AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal	716
Db	1116	GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGACG	1175	Db	1818	GGCTCC-----GGGAGCTCCGCTGGTGGCGAGGACGAGCG-----	1853
QY	358	GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle	377	QY	717	MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	736
Db	1176	GGCAGCGCCAAACCCCAAGGGTGCCATCACTTTGACAAACATCGGTTATGCTTGGATT	1235	Db	1854	-----GATGGGACGGGGCC-----CGGAGCAGCGAGGACGAGCCTCCTCAGAA	1898
QY	378	AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp	397	QY	737	LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer	756
Db	1236	GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGTGGAGATCATGTACTACTGATGGAT	1295	Db	1899	CTGGGAAGGAGGAGGAGGAGGAGGAGCAG-----GCGGATGGGCG	1940
QY	398	AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe	417	QY	757	SerValIleuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp	774
Db	1296	GCTCACTCCTTACAACTTCACTACTTCACTTCACTTCACTATAGTGGGCTCCTTCTTC	1355	Db	1941	GTCTGGCTGTGCGGGATGTGTGGCGGAGACCGCAGCAAGCTGCGCGGCATCTGTGGAC	2000
				QY	775	SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly	794

Db 2001 AGCAAGTACTTCAACCGGGGCATGATGGCCATCTCGGTCAACACCGTCAGCATGGGC 2060
QY IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCGAGCACACGAGCAGCCGGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGGTC 2120
QY PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPropheGly 834
Db 2121 TTCACGACATGTTTGGCCCTGGAGATGCTTGAAGTGGCTGCATTTGGGCTCTTCGAC 2180
QY TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGlu 854
Db 2181 TACCTGGCTAACCCCTACAAACATCTTCGACAGCATCATGTGTATCATCAGCATCTGGGAG 2240
QY IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGGCAGCGGACCGGTGGCTGCTGGTGCTGGGACCTTCCGGCTGCTGGCGGTG 2300
QY LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGGTGGCTTCATGCTCCCTGCGGCGCCAGCTCGTGGTGTCTCATGAAGACC 2360
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Db 2421 CTTGGGATGCATATTTTGGCTGCAAGTTTCAGCCTCCGACGACACTGGAGACACGGTG 2480
QY ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGAACTTCGACTCCTGCTGTGGGCCATCGTCACTGTGTTCAGATCCTC 2540
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Db 2661 GCCATCTGGTGGAGGGCTTCCAGCGGAGGGTGACGCCAATCGCTCCTACTCGGACGAG 2720
QY AspPheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGAGCTCATCCAACATAGAGAGTTTGATAAGTCCAGGAAGGCTGGACAGCAGC 2780
QY GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTCTGCCCAATCCCCATGACCCCCCAATGGGCACCTGGACCCC 2834
QY SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGACCTAGGTCTGTGGGGCTGCGGGACCTGCC--- 2885
QY HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCCGACTCTCACTGCAGCGGACCCCATGCTGTGGTGGCCCTGGGGCTCCCGAAAGAGC 2942
QY SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGTATGTCTCTA-----GGGAGGATGAGCTATGACGAGCGCTCCCTGCTCCAGC 2993
QY AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCCGGAGCTCCTACTACGGGCCCATGGGGCCGCGAGCGCGGCCCTGGGCCAGCGCTCGCTCC 3053
QY SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139

Db 3054 AGCTGGAAC-----AGCCTCAAGCACAAAGCCGCCGTCCGGCGGAGCAT 3095
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QY Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGGCCCGCGCGCGCACCCCTGCACACCCACCCACCCACCCACCATTCATCACGGG 3215
QY -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGCACCCGCCACCCACCACCGCGGACGCTGTCCCTCGACAAACAGGGAC 3275
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QY SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
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QY AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu 1238
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QY 1519 AsnHisAsnProTrpMetLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db AACCACAAACCCCTGGATGCTGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4349
QY 1539 ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln 1558
Db GTGCTCAACATGTTTGTGGGTGTCGTGGTGAGAACTTCCACAAGTGGCGGCAGCACCG 4409
QY 1559 GluGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg 1578
Db GAGGCTGAAGAGGCACGGCGGCGTGAGGAGAAGCGGCTGCGGCGCTGGAGAAAGCGC 4469
QY 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer 1598
Db CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACCTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db CACACCGGCTGCTCATCCACTCCATGTGCACGAGCCACTACCTGGACATCTTCATCAC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db TTTCATCATCTGCCCTCAACGTGGTCAACCATGTCCCTGGAGCACTACAATCAGCCACGTC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTCAACCACTGTCTTTGTGCTGGAGGCT 4688
QY 1659 ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1678
Db GTGCTGAAGCTGGTGGCAATTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db GACCTGGCCATTGTGCTACTGTCTAGTCACTGGGCATCACCTGGAGGAGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db GCGGCCCTGCCCATCAATCCACCATCATCCGCATCATGAGGTTCTGCGCATTGCCCGA 4868
QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db GTGCTGAAGCTGTTGAAGATGGCCACAGGAATGCGGCCCTGCTGGACACGGTGGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAla 1758
Db GCTTTGCCCCAGGTGGCAACCTGGCCCTCCTCTTCATGCTGCTCTTCTTCATCTATGCT 4988
QY 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
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QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db ATGACCGGCATGCCACCTTCGAGAACTTCGGCATGGCCCTTCCTCACACTCTTCCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln 1817
Db TCCACGGGTGACAACTGGAACGGGATCATGAAGGACACGCTGCGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
Db GAGCGCAGCTGCCTGAGCAGCCTGACGTTTGTGTCGCGCTGTACTTCTGAGCTTCGTG 5228

QY 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
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QY 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMet 1875
Db GACAGCAACAAGGAGCGCAGGAGACGCCGAGATGATGATGATGATGATGATGATGATGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly 1894
Db GCGCATGGCTGGCCCTGGCCCGGAGGCTGCCTACCGGTCC----- 5390
QY 1895 ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHis 1914
Db ---CGGGCGCCCTGGCCGAGGCGG--- 5414
QY 1915 IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro----- 1930
Db ---GGAGGGCGGCGCGG---GGGCGACACCGAGGGCGGCTGTGCGCGGCTGTACTC 5470
QY 1931 -----HisProGluGluValProValPro 1938
Db GCCTGCCAGGACTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTGCGGTCCAT 5530
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
Db CTTCCACCCTACTCTCGCTCGCGCTGCGGCTGCAAGAAAGTGTCA-----CCA 5575
QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
Db CGACAA-----GCAAGAGTGCAGCTGGCTGAGACGGA 5608
QY 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
Db GGCCTTCTCCCTGAACTCAGACAGTCTCTGCTCCATCCTGCTGGTGACGACCTGAGTCT 5668
QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
Db CGAGGA-----CCCCACAGCCTG 5686
QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
Db CCCACCTGG-----CCGCAAGGACAGCAAGGTGAGCTGGACCCACCTGAGCCCAT 5737
QY 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla 2045
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QY 2046 IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu 2065
Db ATCCAGAGAACTTCTCTGT--GTGAGATGGAGGAGATCCCCT-----TCAACC 5841
QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIle 2085
Db CTGTCGGTCTCTGGCTGAAACATGACA----- 5868
QY 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
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QY 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
Db CCC-----CGGATGCCTCCAGCC----- 5913
QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu 2145
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QY 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163
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QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183

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QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProProSer 2219
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QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGCCCTGGGGCGCCCGCGCGCTGCTCCAGGACCCCGGGC 6217
QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCCTGTCCCGCGCGCTCGCCGCGCCTGAGCCTGCGCGCGCGGGCCTCTTCAGCCT 6277
QY 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGCGGGCGCATCAGCGCAGCCACAGCAGCGGGGCTCCACCAGCCCGGGCTG 6337

RESULT 11
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 9 Gaps: 63

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QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
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QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGCGCTGGAGGAGCTCTGGATGGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344

QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCCTATTGCCCTTCTTCTGCCTCGACACACACCAGCCCCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCCGTGGTTTGAATGTGTACGATGCTGGTGTATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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QY 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGCAAGATCCTGCAGGTCTTTGATGACTTTCATCTTTATCTTCTTGGCATGGAGATGGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGTACTCCTCGGGGACACATGGAAC 644
QY 186 ArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGGATTCTTCATCGTCATGGCAGGGATGGTTCGAGTACTCCCTGGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
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QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
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QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
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QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
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Db 945 GCCTTGGCCCCCATACTACCAGCGGAGGAGGATGATGAGATGCCCTTTCATCTGCTCCCTG 1004
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QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
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QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTGTGTCAACTGGAACTTACTACAATGTGTGCCGACG 1175
QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCAACCCCCACAAAGGTGCCATCAACTTTGACAACATCGGTTATGCTGGATT 1235
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Db 1236 GTCATCTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGAT 1295
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCACTCCTTCTACAACCTCATCTACTTTCATCTCTGCTTATCATAGTGGGCTCTTCTTC 1355
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Qy	1856	Glus	Asn	Lys	Glu	Ala	Lys	Glu	Ala	Glu	Leu	Glu	Ala	Glu	Leu	Glu	Leu	Glu	Met	1876
		::::																		
Db	5289	GAC	AGCA	CA	AA	GA	GG	CG	CAG	GAG	AC	GC	CG	AG	AT	GC	CG	AG	CT	CGAGATG
Qy	1876	--Lys	Thr	Leu	Ser	Pro	Gln	Pro	His	Ser	Pro	Leu	Gly	Ser	Pro	Phe	Leu	Trp	Pro	---
Db	5349	GCC	CA	TG	GC	CT	GG	CC	CT	GG	CC	CG	AG	GC	TG	CT	AC	CG	GC	CTCCCGGGCGCC
Qy	1894	-----Gly	Val	Glu	Gly	Val	Asn	Ser	Thr	Asp	-----	-----	-----	-----	-----	-----	-----	-----	-----	1902
Db	5406	CG	AG	GG	CC	GG	AG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG
Qy	1903	--Ser	Pro	Lys	Pro	Gly	Ala	Pro	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1917
Db	5466	TAC	TG	CC	CT	GC	-CC	AG	GAG	AAC	CT	TG	GG	CT	GG	AC	AG	CG	TCT	CTTTAATCATCAAGGACTC
Qy	1918	Ala	Ser	Gly	Phe	Ser	Leu	Glu	His	Pro	Thr	Met	Val	Pro	His	Pro	Glu	Glu	Val	ProVal
Db	5525	CT	TG	GAG	GG	--GG	AG	CT	GAC	CA	T-----	-----	-----	-----	-----	-----	-----	-----	-----	5566
Qy	1938	Pro	Leu	Gly	Pro	Asp	Leu	Leu	Thr	Val	Arg	Lys	Ser	Gly	Val	Ser	Arg	Thr	His	Ser
Db	5567	CAT	CT	TCC	ACC	ACT	ACT	CT	CG	CC	TG	CG	GC	TG	CA	AG	AG	TG	TCA	-----
Qy	1958	Pro	Asn	Asp	Ser	Tyr	Met	Cys	Arg	Asn	Gly	Ser	Thr	Ala	Glu	Arg	Ser	Leu	Gly	His
Db	5612	CC	AC	GAC	AA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	5644
Qy	1978	Gly	Trp	Gly	Leu	Pro	Lys	Ala	Gln	Ser	Gly	Ser	Ile	Leu	Ser	Val	His			

Db	6096	TGTACCTCTCTCCGGCAGGCCACCGGAGCGACACGTCGCTGGACGCCAGCCCCAGCAG-	6154
Qy	2199	LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro	2218
Db	6155	CTCCGGGGCAGCCTGCAGACCACGCTCAGGACAGCCTGACCCCTGAGCGACAGCCCCCG	6214
Qy	2219	SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro	2236
Db	6215	GCG-----TGCCCTGGGGCCGCCCGCGCTGCTCCAGACCCCG	6253
Qy	2237	GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer	2256
Db	6254	GGCCGGCCTGTCCCCCGCGCTCGCCGCGCCTGAGCCTGCGCGCGGGGCGCTCTTCAG	6313
Qy	2257	ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly	2276
Db	6314	CCTGGGGGGCTGGGGGGCATCAGCCAGCCACAGCAGCGGGGGGCTCCACCAGCCCCGG	6373
Qy	2277	Leu	2277
Db	6374	CTG	6376

RESULT 12

US-10-425-800-3

; Sequence 3, Application US/10425800

; Publication No. US20030180886A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/10/425,800

; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 6855

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (192).. (6755)

US-10-425-800-3

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QY 1519 AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db 4290 AACCACAACCCCTGGATGCTGTACTTTCATCTCCTTCTGCTCATCTGTCAGCTTCTTT 4349
QY 1539 ValLeuAsnMetPheValGlyValValGluValGluAsnPheHisLysCysArgGlnHisGln 1558
Db 4350 GTGCTCAACATGTTTGTGGGTGCTGGTGGAGAACTTCCACAAGTGC CGGACACAG 4409
QY 1559 GluGluGluGluAlaArgArgGluGluGluLysArgLeuArgArgLeuGluLysLysArg 1578
Db 4410 GAGGCTGAAGAGGCACGGCGGCTGAGGAGAGCGGCTGCGGCGCTGGAGAAGAAGCGC 4469
QY 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer 1598
Db 4470 CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACCTATTGT 4508
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Db 4509 CACACCCGGCTGCTCATCCACTGTCACCGACCGCACTACCTGGACATCTTCATCACC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
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Db 4629 CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCAACCACTGTCTTTGTGTGGAGGCT 4688
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Db 4689 GTGCTGAAGCTGGTGGCATTTGTGCTGAGGCGCTTCTTCAAGGACCGATGGAAACCACTG 4748
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Db 4929 GCTTTGCCCGAGGTGGCAACCTGGGCCCTCCTCTTCATGTGCTCTTCTTCATCTATGCT 4988
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QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
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QY 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
Db 5229 CTCACCCGCGAGTTTCGTGCTCATCAACGTGGTGGTGGCTGTGCTCATGAAGCACCTGGAC 5288

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QY 1894 -----GlyValGluGlyValAsnSerThrAsp----- 1902
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QY 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACGACAA-----GCAAGAGGTGCAGCTGCTGAGAC 5644
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QY 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCGAGGA-----CCCCACAGC 5722
QY 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
Db 5723 CTGCCACCTGG-----CCGCAAGACAGCAAGGTTGAGTGGACCCACCTGAGCC 5773
QY 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATGCGTGTGGAGACCTGGCGGAATGCTTCTTCCCTTGT-CCTCTACGCGCGTCTCGC 5832
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QY 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
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QY 2145 GluProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGGCACTGGAAACCTTCCCCA 6045
QY 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2182
Db 6046 AGATTGGCTG-CAGGGCTCCTGGGCATCT-----CTGCGGTCAACCAAGGGTCAAC 6095
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Db      6155  CTCCGGGGCAGCCTTCAGACCACGCTCGAGGACAGCCTGACCTGAGCGACAGCCCGCG 6214
QY      2219  SerIleSerIleAspProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db      6215  GCG-----TGCCCTGGGGCGCGCGCGCTGCTCCAGGACCCCG 6253
QY      2237  GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
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QY      2257  ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db      6314  CCTGCGGGGCTGCGGGCGCATCAGCGCGCAGCAGCGGGGGCTCCACCAGCCCGGG 6373
QY      2277  Leu 2277
Db      6374  CTG 6376

RESULT 13
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Alignment Scores:
Pred. No.:      0      Length:      6503
Score:          5407.00  Matches:      1234
Percent Similarity: 61.05%  Conservative: 241
Best Local Similarity: 51.08%  Mismatches: 502
Query Match:      44.95%  Indels:      444
DB:              9      Gaps:       60

US-09-611-257A-24 (1-2287) x US-09-935-541-12 (1-6503)
QY      3  ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
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QY      23  SerAspPro-----ProGlyProArgLeuAlaArgGlyTirpThrArgArg 38
Db      115  GCTGATCCGGGAATCCGAGGCGTGGGGCGCGGGG-GCGCGGGGTCCCTCTCCACGCCGG 173
QY      39  Met-----Glu-AlaProArg-----SerArgAspSerProValAla----- 51
Db      174  CTTGGGGACACGCGTCAACCCCGGCTCTGTCCCGGACGACCCCGCTGCGCGGCCACG 233
QY      52  -----SerArgSerSerThrTh 57
Db      234  TCCATGCCAAGGGCTCCCTGCTCCACGCTGACATGGCTGACAGCAACTTACCGCCCTCAT 293
QY      57  rCysProGlyProGly-----AlaAlaGlyAla-GlySerThrG 70

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QY      106  ysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuA 126
Db      474  GCATCAAGATGGTTTGTAAACCGTGGTTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGA 533
QY      126  snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgC 146
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QY 478 yAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498
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QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
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QY 518 isArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyrH 538
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QY 598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlys 618
Db 1713 GCCACTGCAAGCTGTGCCACACGACAGCCCTGGAC----- 1750
QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
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QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAsps 698
Db 1793 -----GCCTCTGACCCCCAGCA 1808
QY 698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyGluProGluS 712
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QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db 1869 CAGGCCAGGAAGGCTCAGGTTCTGTGGTCTCTGCAGAGGCCGAAGCCAATGGGGATGGAC 1928
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Db 1929 TCCAGAGCAGTGAGGATGGGGTCTCCTCGGACCTGGGGAAGGAGGAGGAACAGGAGGACG 1988
QY 750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769
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QY 2051 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu-----ValSerGly 2068
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QY 2106 -----ProCysProGly-----LeuGluPro 2112
Db 6075 AGAAGGGGCAGGAACCGGGCATGATGTCAGGAACCTTGCCCAAG-ATTGCATTTCAGGGG 6133
QY 2113 SerTrpAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu 2131
Db 6134 TCCTGGGATCGCTGAGGTCAACCGAGTGTCAACTGCACCCCTCTTGGCCCGGCTACTGTG 6193

QY 2132 SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAsp 2151
Db 6194 AGTGACACGTCCTTGGATGCCAGTCCTAGCAGCTCA----- 6229
QY 2152 LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgProGlyPheTrpLeu 2171
Db 6229 ----- 6229
QY 2172 AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg 2191
Db 6230 -----GCGGGCAGCTACAGACCACACTGGAAGACAGTCTGACT----- 6268
QY 2192 LeuCysProSerProSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgPro 2211
Db 6269 CTGAGTGACAGTCCCCCGCGTGCCTGGGGCCCGCCGGTCCAGGTGCCTGGG-----CCA 6322
QY 2212 LysLysLysLeuSerProProSerIleSerIleAspProGluSerGlnGlySerArg 2231
Db 6323 CCGGCTAGCCTGTACCGGGCACCCCGCG-----CCGCTCAGCCTGCGGGCGCGTGG 6376
QY 2232 ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247
Db 6377 CCTGTTAGTCTGCGTGGGCTGCGGGCCCATCAGCGTAGCCACAGCAGTGGCGGCTCCAC 6436
QY 2248 -----AspSerLysAspProSer 2253
Db 6437 CAGCCCTGGCTGCACTCACCCAGACTCCATGGACCCCTCT 6476
RESULT 14
US-10-425-800-12
; Sequence 12, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-425-800-12
Alignment Scores:
Pred. No.: 0 Length: 6503
Score: 5407.00 Matches: 1234
Percent Similarity: 61.05% Conservatives: 241
Best Local Similarity: 51.08% Mismatches: 502
Query Match: 44.95% Indels: 444
DB: 16 Gaps: 60
US-09-611-257A-24 (1-2287) x US-10-425-800-12 (1-6503)
QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 64 CCCCCGGGCGCGCCCTGATGCGCGTCCCCCTCGCCCGGGCGCA----- 114
QY 23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTrpThrArgArgArg 38
Db 115 GCTGATCCCGGAATCCGAGCGGTGGGGCGCGGGG-GCGCGGGTCCCTCTCCACGCGG 173
QY 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla----- 51
Db 174 CTTCCGGGACACGCGTCAACCCCGCGTCTCTGCCCCGACGACCCCGCTGCCCGCCACG 233
QY 52 -----SerArgSerSerThrTh 57

Db 234 TCCATGCCAAGGGCTCCCTGTCTCCACGCTGACATGGCTGACAGCAACTTACCGCCCTCAT 293
 QY 57 rCysProGlyProGly-----AlaAlaGlyAla-GlySerThrG 70
 Db 294 CTGCAGACAGCCCGCCCTGAGCCGGGAATCACTGAGCAGCCGGGGCCCCGGAGTCCCC 353
 QY 70 luLysAspProGlySerAlaAspSerGluAlaGluGly-----LeuProTyrP 86
 Db 354 CTCCATCCCTCCAGGCTGGAGAGGCCAATTGGAAGGAACCAACCTGACGTCCACATC 413
 QY 86 roAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTirpC 106
 Db 414 CAGACCTGGCTCCTGTGCTTTCTTCTGCCTGCGCCAGACCACGAGCCACCGAACTGGT 473
 QY 106 ysLeuArgThrValCysAsnProTirpPheGluArgValSerMetLeuValIleLeuLeuA 126
 Db 474 GCATCAAGATGGTTGTAAACCCGTGGTTTCAGTGTGTGAGCATGTGTGGTTATTCTGCTGA 533
 QY 126 snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgC 146
 Db 534 ACTGTGTGACCCCTGGGCATGTACCAGCCATGTGATGACATGGAGTGCCTGTGCGAACCGTT 593
 QY 146 ysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetValV 166
 Db 594 GCAAGATCCTGCAGGTCTTCGATGACTTCATCTTCATCTTCTTTCGATGGAGATGGTGC 653
 QY 166 alLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTirpAsnA 186
 Db 654 TTAAGATGGTGGCCCTGGGCATTTTGGCAAGAGTGTACTACCTCGAGACACATGGAAAC 713
 QY 186 rgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnV 206
 Db 714 GCCTGGATTCTTCATGTTCATGGCAGGGATGGTTGAGTACTCTCTGGACCTACAGAACA 773
 QY 206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV 226
 Db 774 TCAACCTGTACGCCATCCGCACTGTGCGTGTCTGAGGCCTCTCAAAGCCATCAACCCGTG 833
 QY 226 alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnV 246
 Db 834 TACCCAGCATGCGGATCCTGGTGAACCTGTGCTGCACACGCTGCCATGTGGGGAACG 893
 QY 246 alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266
 Db 894 TGCTCCTGCTCTGTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 953
 QY 266 laGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValA 286
 Db 954 CAGGCTGTCTACGGAACGCTGCTTCTCTGGAAGAGAATTTCACCATAAAGGGGATGTGG 1013
 QY 286 spLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306
 Db 1014 CCTGCCCCCTTATTACCAACAGAGAGGATGACGAGATGCCCCCTTATCTGCTCCCTGA 1073
 QY 306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGlyG 326
 Db 1074 CTGGGGACAATGGCATCATGGGCTGCCACGAGATCCCCCACTGAAGGAGCAG----- 1126
 QY 326 lyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSerS 340
 Db 1127 --GGCCGGGAATGCTGCTGTCCAAAGATGATGTGTATGACTTCGGGGCGGGCGCCAGG 1184
 QY 340 erSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaG 358
 Db 1185 ACCTCAACGCCAGCGGTGTGTGCTCAACTGGAACCGCTACTACAACGTCTGCCGACGG 1244
 QY 358 lyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTirpIleA 378
 Db 1245 GCAACGCCAACCCCTCACAAGGGCGCCATCACTTTGACAACATTGGCTATGCCGGGATTG 1304
 QY 378 laIlePheGlnValIleThrLeuGluGlyTirpValAspIleMetTyrPheValMetAspA 398

Db 1305 TGATTTTCCAGGTGATCACTCTGGAAGGCTGGTGGAGATCATGTACTATGTATGGACG 1364
 QY 398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheM 418
 Db 1365 CACATTCTTTCTACAACATTTCATCTACTTCTTCTGCTCATCATAGTGGGCTCCTTCTTCA 1424
 QY 418 etIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
 Db 1425 TGATCAACTTGTGCCTCGTTGTATAGCAACCCAGTTCTCTGAGACCAAGCAACGGGAGC 1484
 QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
 Db 1485 ACCGGCTGATGCTGGAGCAACGCCACCGCTACCTGTCC---TCCAGCACGCTGGCCAGTT 1541
 QY 458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478
 Db 1542 ACCTGAGCCCGGTGATTGCTATGAGGAGATCTTCCAATATGTCTGTACATCCTTCGCA 1601
 QY 478 ysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498
 Db 1602 AAGCCAAGCGC-----CGTGCCCTAGGCCTTACACAGGCCCTG--- 1639
 QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
 Db 1640 -----CAGA 1643
 QY 518 isArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrH 538
 Db 1644 ACCGGCGCCAGGCC----- 1657
 QY 538 isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
 Db 1658 --ATGGGCCCGGGGACA----- 1672
 QY 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
 Db 1673 -----CCAGCCCTGCCAAGCTGGGCC----- 1696
 QY 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
 Db 1697 -----CATGCCAAG-----GAGCCCA 1712
 QY 598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlys 618
 Db 1713 GCCACTGCAAGCTGTGCCACGACACACAGCCCTCTGGAC----- 1750
 QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
 Db 1751 -----CCCACTCCCCACACA----- 1765
 QY 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProp 658
 Db 1766 --CTGGTGCAG----- 1774
 QY 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
 Db 1775 -----CCCATCTCTGCCATTCTG----- 1792
 QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAsps 698
 Db 1793 -----GCCTCTGACCCCAAGCA 1808
 QY 698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyGluProGluS 712
 Db 1809 GCTGCCCTCACTGCCACGACGAGGCGAGGCGGCCCTCTGGCTGGGCGACACTGACT 1868
 QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
 Db 1869 CAGGCCAGGAAGGCTCAGGTTCTGGTGGCTCTGCAGAGGCCGAGCAATGGGATGGAC 1928
 QY 732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749
 Db 1929 TCCAGAGCAGTGAAGTGGGTCTCTCTCGACCTGGGGAAGGAGGAGCAACAGGAGGACG 1988

QY 750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769
 Db 1989 GGG-----CAGCCCGACTGTGTGGG-GATGTGTGGCGGAGACACGAAAAAGCTG 2038
 QY 770 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789
 Db 2039 CGGGGCATCGTGACAGCAAGTACTTCAACAGAGGTATCATGATGGCTATCCTGGTGAAC 2098
 QY 790 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 809
 Db 2099 ACAGTCAGATGGGCATCGAGCACCAAGAACAGCCCGAGAGCTGACCAACATCCTGGAG 2158
 QY 810 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuVal 829
 Db 2159 ATCTGCAATGGGTCTTCAACAGATGTGTGCCCTGGAGATGATCCTGAAACTGGCGGCC 2218
 QY 830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849
 Db 2219 TTTGGGCTCTCGACTACCTGCGGAACCTTACAACATCTTTGACAGCATCATCGTCATC 2278
 QY 850 IleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPhe 869
 Db 2279 ATCAGCATCTGGGAAATCGTGGGCGAGCGGACGGTGGCCCTGTCTGTCTGCGACCTTC 2338
 QY 870 ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal 889
 Db 2339 CGGTTGCTGGGGTGTGAAGCTGGTGGCTTTCATGCCGCGCTGCGGCGCCAGCTCGTG 2398
 QY 890 ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle 909
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 QY 949 ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer 968
 Db 2579 GTGTTCCAGATCTCACTCAGGAGACTGGAACGTTGCTGTGTACAATGGCATGGCCTCC 2638
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 Db 2639 ACCACCCCTGGGCTCCCTCTATTGTTGCCCTCATGACCTTTGGCAACTACGTTCTC 2698
 QY 989 PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys 1008
 Db 2699 TTCAATCTCCTGGTGGCTATCCTGGTAGAGGGTTTCCAGGCTGAGGGTGATGCTAAATCGT 2758
 QY 1009 SerGluSerGluProAspPhePheSerProSerValAspGly----- 1022
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 QY 1023 -----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
 Db 2819 GGCCTGGACAACAGTAGAGATCTCAAGCTCTGCCCAATACCCATGACACCCATGGACAC 2878
 QY 1041 LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet 1058
 Db 2879 CTGGACCTAGCCTC-----CCTCTGGGTGCGCATCTGGGTCTGCTGGTACCATGGGT 2932
 QY 1059 SerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 1078
 Db 2933 ACTGCCCCCGCCTCTCACTGCAGCCAGACCCGGTACTGCTGGGCCCTAGACTCTCGGAAA 2992
 QY 1079 ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProPro 1098
 Db 2993 AGCAGTGTATGTCCTG-----GGCAGGATGAGCTATGATCAGCGCATCTTGTCCTC 3043

QY 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg 1118
 Db 3044 AGCTCCCGAGAGTCTCTACTACGGGCCCTGGGGCCGAGTGGGACCTGGGCTAGCCGCCG 3103
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 Db 3206 CGGAGGAGCGCCCAACTCGCACCGCACCCCTGCATGCTCCACACCGCACCGCGCAC 3265
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 Db 3266 CATGGACCCACCTGGCACACCGTCCACCGACACCAACCGCGGACTCTGTCCCTTGATACC 3325
 QY 1180 LysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer 1199
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 Db 3443 ---ATAGCCAAGGATGCTTTCACCAAGATGGATGATGCCCGCGGACCGCGGGAGGACGAG 3499
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 QY 1297 IlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAla 1316
 Db 3680 ATCTTCTCAACTGTATCACCATTGCTCTGGAGAGACCCAGATTTGAAGCTGGTAGCACT 3739
 QY 1317 GluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMet 1336
 Db 3740 GAGCGCATCTTCTCCTCAGGTGTCTAACTACATCTTTCACAGCCATCTTCTGGGGCAGATG 3799
 QY 1337 ThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSer 1356
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 QY 1357 TrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet 1376
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 QY 1377 ValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThr 1396
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 QY 1397 LeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeu 1416
 Db 3980 TTACGTCCTTTGAGGGTTTATCAGCCGGGGCCCTGGGGTGAAGCTGGTGGTAGAGACGCTC 4039
 QY 1417 MetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIle 1436
 Db 4040 ATCTCCTCCTCAAGCCCATTTGGGAACATCGTCTCTCATGTGTGTCTCTCTCATCATC 4099
 QY 1437 PheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAsp 1456

QY 2113 SerTrpAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu 2131
Db 6134 TCCTGGGCATCGCTGAGGTACCGAGTGTCAACTGCACCCCTCTTGGCGCCAGGCTACTGTG 6193
QY 2132 SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAsp 2151
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QY 2152 LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgProGlyPheTrpLeu 2171
Db 6229 ----- 6229
QY 2172 AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg 2191
Db 6230 -----GCGGGCAGCCTACAGACCACACTGGAGACAGTCTGACT----- 6268
QY 2192 LeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro 2211
Db 6269 CTGAGTGACAGTCCCCGGCGTGCCTGGGGCCGCCGCTCCAGGTGCCTGGG-----CCA 6322
QY 2212 LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231
Db 6323 CGGGCTAGCCTGTACCGGCCACCCCGCG-----CCGCTCAGCCTGCGGGGCGGTGG 6376
QY 2232 ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247
Db 6377 CCTGTTTAGTCTGCGTGGGTGCGGGCCCCATCAGCGTAGCCACAGAGTGGCGGCTCCAC 6436
QY 2248 -----AspSerLysAspProSer 2253
Db 6437 CAGCCCTGGCTGCACTCACCACGACTCCATGGACCCCTCT 6476

RESULT 15

US-09-030-482B-18
; Sequence 18, Application US/09030482B
; Patent No. US2002000972A1
; GENERAL INFORMATION:
; APPLICANT: Snutch, Terry
; APPLICANT: NeuroMed Technologies, Inc.
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030,482B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 60/039,204
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5562)
; OTHER INFORMATION: Human alpha-1 partial sequence from BAC bK206c7
US-09-030-482B-18

Alignment Scores:

Pred. No.: 0 Length: 5562
Score: 3950.00 Matches: 905
Percent Similarity: 55.52% Conservative: 167
Best Local Similarity: 46.87% Mismatches: 353
Query Match: 32.84% Indels: 506
DB: 9 Gaps: 45

US-09-611-257A-24 (1-2287) x US-09-030-482B-18 (1-5562)

QY 59 ProGlyProGly-----AlaAlaGlyAlaGlySerThrGlu 70
Db 226 CCTGGAAACAGGATGCACACGGGACCTTCCAGGAAGGAGCTGAGCCTGGTTTCATCTCAG 285

QY 71 LysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaPro 90
Db 286 CACCCTGAGGCACAGGCCACGTATACAGCAGGGTGCACCCAGCCCCACGGGCGATCCC 345
QY 91 ValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrVal 110
Db 346 ACCTGCTGCTTTGTCTTGAC-----TTGGTG 372
QY 111 CysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeu 130
Db 373 TGCACG--TGGTTTGAATGTGTGAGCATGTGGTGTATCTGCTGAACCTGCGTGACACTT 429
QY 131 GlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGln 150
Db 430 GGCATGTACCAGCCGTGCGACGACATGGACTGCCCTGTCCGACCGCTGCAAGATCCTGCAG 489
QY 151 AlapheAspAspPheIlePheAlaphePheAlaValGluMetValValLysMetValAla 170
Db 490 GTCTTTGATGACTTCATCTTTATCTTCTTTGCCATGGAGATGGTGTCTCAAGATGGTGGCC 549
QY 171 LeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePhe 190
Db 550 CTGGGATTTTGGCAAGAAGTGTACTCTCGGGGACACATGGAACCGCTGGATTCTTCTTC 609
QY 191 IleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAla 210
Db 610 ATCGTCATGGCAGGC-----AACATCAACCTGTGAGCC 642
QY 211 ValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArg 230
Db 643 ATCCGCACCGTGGCGTCTTGAGGCCCTCTCAAAGCCATCAACCGCGTGCCAGTATGCGG 702
QY 231 IleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCys 250
Db 703 ATCCTGGTGAACCTGCTCTCTGGACACACTGCCCATGTGGGGAATGTCTGTCTGTCTGC 762
QY 251 PhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArg 270
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QY 271 AsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyr 290
Db 823 AACCGCTGCTTCTTGAGGAGAACTTCACCATACAAGGGGATGTGGCCTTGCCCCCATAC 882
QY 291 TyrGlnThrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGly 310
Db 883 TACCAGCGGAGGAGGATGATGAGATGCCCTTCATCTGCTCCCTGTTCGGGCGCAATGGG 942
QY 311 MetArgSerCysArgSerValProThrLeuArgGlyGluGlyGlyProProCys 330
Db 943 ATAATGGGCTGCCATGAGATCCCGCCCTCAAGGAGCAG-----GGCCGTGAGTGC 993
QY 331 SerLeu-----AspTyrGluThrTyrAsnSerSerSerAsnThrThr 344
Db 994 TGCCTGTCCAAGGACGACGCTCTACGACTTTGGGGCGGGGCGCCAGGACCTCAATGCCAGC 1053
QY 345 -----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnPro 362
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QY 363 PheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnVal 382
Db 1114 CACAAGGTTGCCATCAACTTTGACAACATCGGTTATGTTGGATTGTCTTCCAGGTG 1173
QY 383 IleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyr 402
Db 1174 ATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGATGCTCACTCTCTTCTAC 1233
QY 403 AsnPheIleTyrPheIleLeuLeuIleIle----- 412
Db 1234 AACCTCATCTACTTTCATCTCTGCTTATCATTAAGTGAGCTCATCCACCTCGTCATGCTGAC 1293
QY 412 ----- 412

Db	1294	TGCAGCTTCAGCACAGCAGAGTCCCCAAATGTCAAGGTATTCACTCCAGGAGTCGCT	1353	Db	2146	TCC-----	2160
QY	412	-----	412	QY	673	ThrGlyAlaCys--HisSerSerCysLysIleSerSerProCysSerLysAlaAspSer	691
Db	1354	GCTGAATCCCTGCTGCGAGACTCTAGCTCCTCAGTCATCACTGATGAGGCTGCAGCC	1413	Db	2161	TGCCCTTGCTGCCAGCATGAGGACGGCGCGGCCCTCGGGCTGGCAGCACCGACTCG	2220
QY	412	-----	412	QY	692	GlyAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGlu	711
Db	1414	ATGGAGAACCTCCTGGCGGCACCTCCAAGGGGATGAAAGCTATCTGCTCAGGCTGGCC	1473	Db	2221	GGCCAGGAGGGCTCGGGCTCC-----GGGAGCTCGCTGGTGGCGAGGACGAG	2268
QY	412	-----	412	QY	712	SerAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAsp	731
Db	1474	GGCAGCCAAGTTCACTCCAGGCTCAGCAATGCTGGGAGGGGGCTGGGCCCTGAAAGC	1533	Db	2269	GCG-----GATGGGACGGGGC-----CGGAGCAGCGAGGAC	2301
QY	412	-----	412	QY	732	AlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyPro	751
Db	1534	CTGGAAACTGGAGAGGAGCCCCACTCGTGGAGCCCTCGGGCCACAAGGAGATGGGATCCC	1593	Db	2302	GGAGCCTCCTCAGAACTGGGGAAGGAGGAGGAGGAGGAGGAGCAG-----	2346
QY	413	-----ValGlySerPhe	416	QY	752	AspAlaGluProSerSerValLeuAla-----PheTyrArgLeuIleCysAspThrPhe	769
Db	1594	CAATGCCAACCAAGGCAGCCTCTCCCCCTTCATTTCATGCAAGCACAGGTGGCTCCTTC	1653	Db	2347	---GCGGATGGGCGGTCTGGCTGTGCGGGGATGTGTGCGGGAGACGGGAGCCAAGCTG	2403
QY	417	PheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArg	436	QY	770	ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn	789
Db	1654	TTTCATGATCAACCTGTGCTCGTGTGTATAGCGACCCAGTTCTCGGAGACCAAGCAACGG	1713	Db	2404	CGCGGCATCGTGGACAGCAAGTACTTCAACCGGGGCATCATGATGGCCATCCTGGTCAAC	2463
QY	437	GluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAla	456	QY	790	ThrLeuSerMetGlyIleGluTyrHisGluGlnProGlu-----	802
Db	1714	GAGCACCGGCTGATGTGGAGCAGCGGCAGCGCTACCTGTCC---TCCAGCACGGTGGCC	1770	Db	2464	ACCGTCAGCATGGGCATCGAGCACCAAGCAGCAGGCCAGTGCAGCGCAGCGGGCGGGGCC	2523
QY	457	SerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrIleLeu	476	QY	803	-----GluLeuThrAsnAlaLeuGlu-----	809
Db	1771	AGCTAGCGCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCCTG	1830	Db	2524	TGCGGAGAGGACAAAATCCAGACCTTTGCATGACCCCTCAAGGCCCTTGTCTGTGTAC	2583
QY	477	ArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeu	496	QY	810	-----IleSerAsnIleVal-----	814
Db	1831	CGCAAGGCCAAGCGC-----CGCGCCCTGGGCTCTACAGGCCCTG	1872	Db	2584	AACGTCCCTTCACCAGGCCAGGGTGTCTGTCCCATCCAGTGACTCCACCCCATACAGCC	2643
QY	497	LeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArg	516	QY	814	-----	814
Db	1873	CAGAGCCGGCGCCAGGCCCTGGGCCCGGAGGCCCGGCCCGCC-----	1917	Db	2644	CCATGGCGCATGGAGACAGGAAAGCAGGGACACGGATGTGAAGAGGACCAGGACAACGA	2703
QY	517	SerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHis	536	QY	815	PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGly	834
Db	1917	-----	1917	Db	2704	AGCAGTGACATGTTGCCCTGGAGATGATCCTGAAGCTGGCTGCATTTGGGCTCTTCGAC	2763
QY	537	TyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArg	556	QY	835	TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyrGlu	854
Db	1917	-----	1917	Db	2764	TACCTGCGTAACCCCTACAACATCTTCGACAGCATCATTTGTTCATCATCAGCATCTGGGAG	2823
QY	557	AspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGly	576	QY	855	IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal	874
Db	1918	-----AAACTGGGCCCCCAGCCCAAGGAGCCCCCGGCAC	1950	Db	2824	ATCGTGGGCAGGCGGACGGTGGGCTGTGCGGTGCTCGGACCTTCGCGCTGCTGCGCGTG	2883
QY	577	GlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGlu	596	QY	875	LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr	894
Db	1951	TACCTCTCACAGTCTGGGAATCGATTCTTGGGAGGCAAGCAGAGAATGCACGCTC---	2007	Db	2884	CTGAAACTGGTGGCTTCATGCCTGCCCTGCGCGCCAGCTCGTGGTGTCTCATGAAGACC	2943
QY	597	ProValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrVal	616	QY	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle	914
Db	2008	-----AGAGCTGCCGCCACCCCG-----	2025	Db	2944	ATGGACAACGTGGCCACCTTCTGCATGCTGTCTCATGCTCTTCATCTTCATCTTCAGCATC	3003
QY	617	GlySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAsp	636	QY	915	LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu	933
Db	2026	TCCTCGGTGCCAGCCATCCAGCGTGGGCTCGGAGGAGGCCCCAGAGCTGTGCCCGCAA	2085	Db	3004	CTTGGGATGCATATTTTGGCTGCAAGTTCAGCCTCCGCACGGACACTGGAGACACCGGTG	3063
QY	637	LysAlaLeuValGluValAlaPro-----SerProGlyProProThrLeuThr	652	QY	934	ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu	953
Db	2086	CATAGCCCCCTGGATGGACGCCCCACACCCCTGGTGCAGCCCATCCCGCCACCGTGGCT	2145	Db	3064	CCCACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGTCACTGTGTTCAGATCCTC	3123
QY	653	SerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSer	672	QY	954	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	973
		---		Db	3124	ACCCAGGAGGACTGGAAACGTGTTTCTTACAATGGCATGGCCCTCCACTTCTCCCTGGGCC	3183

QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 3184 TCCCTCTACTTGTGCGCCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTGCTGGTG 3243
QY 994 AlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 3244 GCCATCTGTTGGTAGGGCTTCCAGCGGAGGTGACTGTGGTCTTGGCAGAGGAACACCC 3303
QY 1003 ----- 1003
Db 3304 CCACAGGCCTCGAAAGACTGGGCGAGGAGAGGTGGCTGGATGGGGAGGGCTGCAA 3363
QY 1004 -----GlyAsp 1005
Db 3364 TTCAAACCTTAGCAGGCAACCTATCCCTAAAGAGGGGGTGTGATGAGTGGGTGAC 3423
QY 1006 AlaThrLysSerGluSerGluProAspPhePheSerProSerVal----- 1020
Db 3424 GCCAATCGCTCCTACTCGGACGAGGACCAGAGCTCATCCAACATAGAAGAGTTGATAAG 3483
QY 1021 -----AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeu 1035
Db 3484 CTCACGAGAGGCCTGGACAGCAGCGGAGATCCCAAG-----CTCTGCCCCAATCCCCATG 3537
QY 1036 GlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisThr----- 1053
Db 3538 ACCCCCAATGGGCACCTGGACCCAGTCTC-----CCTGGGTGGGCACCTAGGTCTCT 3591
QY 1054 -----AlaAlaThrPro----- 1057
Db 3592 GCTGGGGCTGCGGGACCTGCCCCCGGACTCTCACTGCAGCGGACCCCATGCTGGTGGCC 3651
QY 1058 MetSerHisProLysSerSerSerThrGlyValGly-----GluAla 1071
Db 3652 CTGGGCTCCCGAAGAGCAGCGCTCATGCTCTAGGGAGGATGAGCTATGACCAGCGCTCC 3711
QY 1072 LeuGlySerGlySerArgArgThrSerSerSerGlySerAla----- 1085
Db 3712 CTGGTGGTGGTCTTAGAGCCACAGCGGGGTGCAGGCTGCCTTTGGGCACCTGGTGCCC 3771
QY 1086 GluPro-----GlyAlaAlaHisHisGluMetLysCysProSerAla 1100
Db 3772 CAGCCGTGGGTGCTGTGGGCGCTGACCCGAACGGGAACCTCTTCCAGTCCAGCTCC 3831
QY 1101 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSerSer 1120
Db 3832 CGGAGCTCCTACTACGGGCCATGGGGCCGCGAGCGCGGCTGGCCAGCGCTCGCTCCAGC 3891
QY 1121 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1140
Db 3892 TGGAAC-----AGCCTCAAGCACACAGCCCGCTCGCGGAGCATGAG 3933
QY 1141 SerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu 1159
Db 3934 TCCCTGCTCTCTGCGGAGCGCGCGCGCGCGGCTGCGGAGGTGGCCGCGGACGAG 3993
QY 1160 -----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3994 GGGCCGCGCGGGCGCGACCCCTGACACCCCAACAGCCACACGCTTTCATCAGGGGCC 4053
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSer 1182
Db 4054 CATCTGGCGCACCGCCACCGCCACCGCGGACGCTGCTCCCTCGACACACAGGACTCG 4113
QY 1183 PheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgSer 1202
Db 4114 GTGACCTTGGCCGAGCTGGTGGCCCGGTGGCGCGCCACCCCGCGCGCTGGAGGCG 4173
QY 1203 Ser-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1220
Db 4174 GCAGGCCCGGCCCGCGCATGAGGACTGCAATGGCAGGATGCCCAGC-----ATCGCC 4227

QY 1221 ArgThrLeuArgThr-----AspAspProGlnLeuAspGlyAspAspAsnAsp--- 1237
Db 4228 AAAGACGTCTTACCAAGATGGGCGACCGCGGGATCGCGGGAGGATGAGGAGAAATC 4287
QY 1238 -----GluGlyAsnLeuSerLysGlyGluArgIleGlnAla 1249
Db 4288 GACTACGTGAGTGGGGCGGGCCGAAGGGACCTGACCTGTCTTCCGCGTCGCAAG 4347
QY 1250 TrpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIle 1269
Db 4348 ATGATCGACGCTATAAGCCCGACTGGTGGAGGTCCGGAAGACTGGTCTGTACCTC 4407
QY 1270 PheProProGlnSerArgPheArg-----LeuLeuCys----- 1280
Db 4408 TTCTCTCCCGAGAACAGGCTCAGGGATCTGGGCTGGGTAAAGCTCGAGTCCAGGAAAG 4467
QY 1281 -----HisArgIleIleThr 1285
Db 4468 GTGGGTGACCTCGTGGTGTGGGTGTATGGTCAAGAGGCGAGCCCATATTATGCC 4527
QY 1286 HisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAla 1305
Db 4528 CACAAACTCTTCGACTACGTGCTCTGGCCTTTCATCTTCTCAACTGCATCACCATCGCC 4587
QY 1306 MetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsn 1325
Db 4588 CTGGAGCGGCTCAGATCGAGGCGGCGAGCACCGAAGCGCATCTTCTCACCGTGTCCAAC 4647
QY 1326 TyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrp 1345
Db 4648 TACATCTTCAGGGCCATCTCGTGGCGGAGATGACATTGAAGGTAGTCTCGTGGGCTG 4707
QY 1346 CysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuVal 1365
Db 4708 TACTTCGGCGAGCAGGCGTACCTACGCAGCAGCTGGAACGTGCTGGATGGCTTCTTGTG 4767
QY 1366 LeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeu 1385
Db 4768 TTCGTGTCCATCATCGACATCGTGGTGTCCCTGGCCTCAGCCGGGGAGCCAAAGATCTG 4827
QY 1386 GlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArg 1405
Db 4828 GGGGTCTCCGAGTCTTGGCGTCTCTGCGCACCTACGCCCTTACGCCCTGCGTGTCTCAGCCGG 4887
QY 1406 AlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsn 1425
Db 4888 GCGCGGGGCTGAAGCTGGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAAC 4947
QY 1426 IleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPhe 1445
Db 4948 ATCGTGTCTCATCTGTGTGCTTCTTCATCATCTTTGGCATCTCTGGGAGTGCAGCTCTTC 5007
QY 1446 LysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAsp 1465
Db 5008 AAGGCAAGTTCTACCACTGTCTGGGCGTGGACACCGCAACATCACCAACCGCTCGGAC 5067
QY 1466 CysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGln 1485
Db 5068 TGCATGGCGGCCAACTACCGCTGGTCCATCACAATAACAATTCGACAACCTGGGCCAG 5127
QY 1486 AlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAsp 1505
Db 5128 GCTCTGATGTCCCTCTTTGTCTGTCATCCAAGGATGGTGGTGAACATCATGTACAAT 5187
QY 1506 GlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeu 1525
Db 5188 GGACTGGATGCTGTGTGTGGACCGAGCGCTGTGACCAACCAACCCCTGGATGCTG 5247
QY 1526 LeuTyrPheIleSerPheLeuIleValAlaPheValLeuAsnMetPheValGly 1545
Db 5248 CTGTACTTCATCTCCTTCCTGCTCATCGTCAAGTCTTGTGTCTCAACATGTTGTGGGT 5307
QY 1546 ValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArg 1565

Db	5308	GTGCGTGGAGAACTTCCACAAGTGC	CGGAGCAC	CAGGAGGCTGAAGAGGCACGGCGG	5367
Qy	1566	ArgGluGluLysArgLeuArgArgLeu	GluLysLysArgArgSerLysGluLys	GlnMet	1585
Db	5368	CGTGAGGAGAGCGGCTGCGGCGCCT	TGGAGAAGAAGCGCCGG	-----	5409
Qy	1586	AlaGluAlaGlnCysLysProTyrTyr	SerAspTyrSerArgPheArgLeuLeu	ValHis	1605
Db	5410	---AAGGCCCAAGCGGCTGCCCTACT	ATATGCCACCTATTGTACACCCGGCT	GCTCATCCAC	5466
Qy	1606	HisLeuCysThrSerHisTyrLeuAsp	LeuPheIleThrGlyValIleGlyLeu	AsnVal	1625
Db	5467	TCCATGTGCACCCAGCCACTACCT	TGGACATCTTCATCACCTTTCATCAT	TCTGCCTCAACGTG	5526
Qy	1626	ValThrMetAlaMetGluHisTyrGln	GlnPro	1636	
Db	5527	GTCACCATGTCCCTGGAGCACTACA	ATCAGCCC	5559	

Search completed: April 28, 2005, 20:02:02
Job time : 2352 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 28, 2005, 07:20:16 ; Search time 9634 Seconds
(without alignments)
9036.017 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR.....KKDTLSLSGLSSDPTMDPZ 2287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09611257/runat_26042005_150449_14906/app_query.fasta_1.2439
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257@cgn_1_1.6069@runat_26042005_150449_14906 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1719.5	14.3	6636	3 BC043482	BC043482 Mus muscu
2	1698	14.1	6035	3 BC051413	BC051413 Mus muscu
3	1406	11.7	990	4 BI905383	BI905383 603167426
4	1385.5	11.5	939	4 BI736618	BI736618 603361089
5	1343	11.2	1076	4 BM479323	BM479323 AGENCOURT
6	1300	10.8	1064	4 BM451648	BM451648 AGENCOURT
7	1293.5	10.8	5666	9 AY416501	AY416501 Mus muscu
8	1275	10.6	879	7 CF548698	CF548698 AGENCOURT
9	1256.5	10.4	793	6 CA319705	CA319705 UI-M-FW0-

10	1230.5	10.2	5943	9 AY416499	AY416499 Homo sapi
11	1198	10.0	715	7 CF745071	CF745071 UI-M-GV0-
12	1197	10.0	810	5 BU709095	BU709095 UI-M-EW0-
13	1195.5	9.9	952	7 CF584866	CF584866 AGENCOURT
14	1190.5	9.9	4675	3 AK083220	AK083220 Mus muscu
15	1187.5	9.9	771	5 BU058818	BU058818 UI-M-FR0-
16	1185	9.9	736	4 BI160856	BI160856 602864778
17	1182	9.8	711	5 BM950154	BM950154 UI-M-EH0p
18	1172	9.7	777	5 BU708898	BU708898 UI-M-FI0-
19	1163.5	9.7	957	4 BG298038	BG298038 602396253
20	1162.5	9.7	777	6 CA945335	CA945335 UI-M-FD0-
21	1141	9.5	973	2 BF783704	BF783704 602109506
22	1140.5	9.5	828	2 BF606929	BF606929 MY2_00012
23	1136.5	9.4	784	7 CF742232	CF742232 UI-M-HB0-
24	1135	9.4	690	6 CB840838	CB840838 M15E-1247
25	1112	9.2	6822	9 AY406058	AY406058 Mus muscu
26	1111	9.2	6813	9 AY406056	AY406056 Homo sapi
27	1103.5	9.2	845	6 CA327685	CA327685 UI-M-FY0-
28	1102.5	9.2	773	4 BI249987	BI249987 602995228
29	1096	9.1	676	4 BI917129	BI917129 603181539
30	1088.5	9.0	727	5 BQ443110	BQ443110 UI-M-EV0-
31	1088	9.0	710	7 CR576255	CR576255 CR576255
32	1079.5	9.0	647	6 CB518482	CB518482 UI-M-GH0-
33	1075	8.9	667	7 CF531859	CF531859 UI-M-GH0-
34	1074.5	8.9	731	7 CN534628	CN534628 UI-M-HS0-
35	1067	8.9	707	7 CN216936	CN216936 RJA002G02
36	1061.5	8.8	708	5 BQ179746	BQ179746 UI-M-EW0-
37	1059	8.8	693	5 BM949227	BM949227 UI-M-EG0p
38	1055.5	8.8	803	6 CB245297	CB245297 UI-M-FY0-
39	1034	8.6	843	5 BQ180375	BQ180375 UI-M-EX0-
40	1032.5	8.6	710	5 BU704267	BU704267 UI-M-FO0-
41	1018.5	8.5	684	5 BU262763	BU262763 603374462
42	1012	8.4	772	6 CB524438	CB524438 UI-M-FY0-
43	1011	8.4	652	2 BB660642	BB660642 BB660642
44	1009	8.4	640	6 CB056097	CB056097 NISC_jj12
45	997.5	8.3	658	5 BQ109588	BQ109588 imageqc_7

ALIGNMENTS

RESULT 1
BC043482
LOCUS BC043482 6636 bp mRNA linear HTC 19-NOV-2003
DEFINITION Mus musculus calcium channel, voltage-dependent, alpha 1F subunit, mRNA (cdna clone IMAGE:5369391), containing frame-shift errors.
ACCESSION BC043482
VERSION BC043482.1 GI:28175783
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 6636)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Db 1251 TGAGCTGCCTTGGGTGTACTTTGTGAGCCTTGTCATCTTTGGGTCTCTTCTTTGTCTCTCAA 1310

Qy 420 nLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLe 440

Db 1311 CCTTGCTTGGAGTCTTAAGCGGGAGTTCTCCAAGGAAGAGAAAAGGCAAAAGCACG 1370

Qy 440 uMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG1 460

Db 1371 AGGTGACTTTCAGAAGCTTCGG-----GA 1394

Qy 460 uProGlySerCysTyrgluGluLeuLeuLysTyrlEuValTyrlleLeuArgLysAlaA1 480

Db 1395 GAAGCAGCAGATGGAAGAAGACCTTCGGGGCTACCTGGGACTGGATCACACAGGCTGAGGA 1454

Qy 480 aArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPr 500

Db 1455 GTTAGACCTTCATGACCCCTCA-----GTAGACGGCAACTTGGCTTCT----- 1497

Qy 500 oValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgAr 520

Db 1498 -CTTGCTGAAGAGGGACGG-----GCGGGCCATCGTAG 1529

Qy 520 gLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuG1 540

Db 1530 G-----CAACTCAA 1538

Qy 540 yAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAlaAsnG1 560

Db 1539 TTCCTGGCCCGCTTC-ATTCCT-----AGCCCTGATGTG----- 1571

Qy 560 ySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPro-- 579

Db 1572 ----ATTGCCCTCCTGAAACCCAGACCAAGCCTGCAGCCACCCTA-GGCTTTGCCCCAAA 1626

Qy 580 -----ArgGlyAlaGluSerValHisSerPheTyrlHisAlaAspCysHisLeuGluPr 597

Db 1627 TCTGGATCAGGGCACAGAATCTCAACCCAGATTTCAGATACAAGACTC-CAACTAGTTCC 1685

Qy 597 oValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValG1 617

Db 1686 T-----TGTCCTTAGATTGACC----- 1704

Qy 617 ySerGlyLysValTyrlProThrValHisThrSerProProProGluIleLeuLysAspLy 637

Db 1705 -----CTAATTCTGCCACCACGCACTCTTCTCAG----- 1734

Qy 637 sAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePr 657

Db 1735 -----TTACAACATATCCCCCACA---GGGCCACAACCTGCAGAGCTGACCAATAGGAG 1784

Qy 657 oProGlyPro-----PheSerSerMetHisLysLeuLeuGluThrGlnSerThrG1 674

Db 1785 GCGGGACGGCTGCGATGGTTTCAGC-----CACTCTACTCGCTCCACACTCCACCAG 1838

Qy 674 yAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCy 694

Db 1839 CAGC---CAGCCAGCCTCCCAGCCAGTGACACTGGCTCCATGACAGACACC----- 1887

Qy 694 sGlyProAspSerCysProTyrlCysAlaArgThrGlyAlaGlyGluProGluSerAlaAs 714

Db 1888 -----CCTGGAGATGAGGATGAAGAAGA-GGGGA 1915

Qy 714 pHis-----ValMetProAspSerAspSerGluAlaValTyrlGluPheThrG1 730

Db 1916 CCATGGCTAGCTGTACACGCTGCCT-----AAACA 1945

Qy 730 nAspAlaGlnHisSerAspLeuArgAspPro-HisSerArgArgArgGlnArgSerLeuG 750

Db 1946 AGATTATGAAAACAAGGATCTG-----CCGCCACTTCGCGCCGAGCCAAACCGGGGTCTC- 1998

Qy 750 lyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhea 770

Db 1999 -----CGTGCACGCTGC-----C 2011

Qy 770 rgLysIleValAspSerLysTyrlPheGlyArgGlyIleMetIleAlaIleLeuValAsnT 790

Db 2012 GCCGGGCGGTCAAGTCCAAAGCCTGCTACTGGGCTGTACTGTGTCTCTTCTCTCAACA 2071

Qy 790 hrLeuSerMetGlyIleGluTyrlHisGluGlnProGluGluLeuThrAsnAlaLeuGluI 810

Db 2072 CGTTGACCATAGCTTCAGAGACCACTGGGCAGCCCTTTGTGGCTCACCCAGACCCAAAGAGT 2131

Qy 810 leSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValT 830

Db 2132 ATGCCAAACAAAGTTCTGCTCTGCCTCTTCACTGTGGAGATGCTCTCAAACTGTACGGCC 2191

Qy 830 yrGlyProPheGlyTyrlIleLysAsnProTyrlAsnIlePheAsp-----G 845

Db 2192 TGGGCCCTCTGTCTACGTTGCCTCTTTTCAACCGCTTTGACTGCTTCGTGCTGTGTG 2251

Qy 845 lyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerV 865

Db 2252 GGGGCATCCTAGAAACCACTTTGGTGGAGGTGGGGGCCATGCAGCCTCTTGGCATCTCAG 2311

Qy 865 alLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuG 885

Db 2312 TGCTCGATGTGTACGTCCTCAGGATCTTCAAGGTCAACAGGCACACGACCTGGGCATCCCTGA 2371

Qy 885 lnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuL 905

Db 2372 GCAATCTGGTGGCATCTTTGCTCAATTCCATGAAGTCCATCGCCTCCTTGTGCTTCTCTCC 2431

Qy 905 euMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheA 925

Db 2432 TCCTTCTCTCATCATCTCTCTCCCTGCTTGGCATGCAGCTGTTTGGGGCAAGTTCA 2491

Qy 925 laSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpA 945

Db 2492 ACTTTGACCAG-----ACCCACACCAAGAGGAGCACCTTTGATACCTTCCCCCAAG 2542

Qy 945 lalleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrlAsnG 965

Db 2543 CCCTCTCACTGTCTTTTCAGATCCTGACTGGTGAGGATGGAACGTTGTTCATGTATGATG 2602

Qy 965 lyMetAlaSer-----ThrSerSerTrpAlaAlaLeuTyrlPheIleA 979

Db 2603 GTATCATGGCCCTACGGTGGGCCCTTCTTCCCAGGGATGCTGGTGGTGTATTATTCATCA 2662

Qy 979 laLeuMetThrPheGlyAsnTyrlValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999

Db 2663 TCCTCTCATCTGTGGCAACTACATCCTGTGAACGTGTTCTTGCCATTGCCGTGGATA 2722

Qy 999 lyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPheSerProS 1019

Db 2723 ACCTA--GCCAGCGGGATGCAGGCACTGCCAAA----- 2754

Qy 1019 erValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039

Db 2755 -----GACAAGGCCAGAGAGAAG----- 2772

Qy 1039 laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometS 1059

Db 2773 -----AGCAGTGAAGGAA 2785

Qy 1059 erHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT 1079

Db 2786 ACCCTCCAAAGGAGAACAAAGTATTGGTG----- 2814

Qy 1079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProS 1099

Db 2815 -----CCTGGTGGAGAGAATGAGGACGCAAG-----G 2842

Qy 1099 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1119

Db 2843 GTGCAAGAAGTGAA----- 2856

Db 4784 GGAATCGATGTGACCTGAGTCTGACTTTGGCCAGGCGAGGAATTTACCTGT---GGT 4840

Qy 1824 ThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuVal 1843

Db 4841 AGCAGTTTGGCCATCGTCTACTTCATCAGCTTCTTTATGCTCTGTGCTTCTCGATTATA 4900

Qy 1844 AsnValValIleAlaValLeuMet----- 1851

Db 4901 AATCTCTTTGGGCTGTAATCATGATAAATTTTGATTACCTAAACCAGAGATTGGTCTATC 4960

Qy 1852 -----LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGlu 1868

Db 4961 CTGGGACCCCAACCACTTGATGAATTC--AAGAGGATCTGGTCTGAATATGACCCCGGA 5017

Qy 1869 AlaGluLeuGluLeuGlu-----MetLysThrLeuSerProGln 1881

Db 5018 GCCAAGGGCCGCATCAAGCACTTGGATGTGGTTGCCCTGCTGAGACGCATCCAGCCCCCA 5077

Qy 1882 -----ProHisSer----- 1884

Db 5078 TTGGGATTTGGAAGCTATGCCCAACACCGAGTGGCTGCAAGAGACTCGTGGCAATGAAT 5137

Qy 1885 ---ProLeuGlySerProPhe-----LeuTrpProGlyVal 1895

Db 5138 GTGCCCTCAACTCAGA-TGGAACAGTGACATTCAACGGCTACACTCTTTGGCCCTGGTGCG 5196

Qy 1896 GluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIle 1915

Db 5197 GACATCCCTGAAGATCAAGACAGAGGAACCTGGATCAAGCAACCAACGAGGCTTCGGAT 5256

Qy 1916 GlyAlaAlaSerGlyPheSerLeuGluHisProThrMetVal-----ProHisProGlu 1933

Db 5257 GGTCAATCAAAAAGATCTGGAAGCGGATAAGCAGAAATTTGTGGATGAGGTATCCCTCC 5316

Qy 1934 -----GluValProValPro---Leu 1939

Db 5317 TCCCGATGAGGAGGAGTCACTGTGGGAAAATTTCTATGCCACATTCCTGTATCCAAGATTA 5376

Qy 1940 GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsn 1959

Db 5377 TTTCCGAAAATCCGGAGAAGGAAGAAAGGGGCTACTAGGAAGAGAGGC---CCCAAC 5433

Qy 1960 AspSerTyrMetCysArgAsnGlySerThrAlaGluArgSer----- 1973

Db 5434 AAGCACATCTCTGCCCTCCAGGCTGGTCTAAGGAGCCTGCAGGACTTGGGTCTCTGAGAT 5493

Qy 1974 -----LeuGlyHisArgGlyTrpGlyLeuProLysAlaGln 1985

Db 5494 CCGTCAAGCCCTCACCTATGACACTGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5553

Qy 1986 SerGly-----SerIleLeuSerValHisSerGln 1995

Db 5554 GGAGGCTGAGGAAGAGGAAGCTGAGAACACCCAGAACCATACAAAGACTCCATAGACTC 5613

Qy 1996 ProAla-----AspThrSerCysIleLeuGlnLeuProLysAsp 2008

Db 5614 CCAGCCCAATCTCGATGGAACCTTAGGATTT-CGGTGTCTCTACCTGTTAAGGAGAAAC 5672

Qy 2009 ValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPro 2028

Db 5673 TTCCAGATTCTCTCTCAACTGGGCGGAGTGATGATGGGC-----TGCGTCCCA 5723

Qy 2029 ProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThr 2048

Db 5724 ACTCCAGGC--AGCCCCAGTGTGTATACAGGCTGGCTCCCAACCAACACA----- 5768

Qy 2049 AspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGly 2068

Db 5769 -----GGAGAAGCTCTGGGG 5783

Qy 2069 ProSerCysProLeuThrArg-----SerSerSerPheTrpGlyGlySer 2083

Db 5784 TTTTCATGTTCACTATCCCGGAAGAGGAAGTATTTCAGCTCAAGGGAACTCAAGGGCAGG 5843

Qy 2084 SerIleGlnValGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeu 2103

Db 5844 ACAATCAGATGAGGAACAGGAAGTCCCTGACTGGACTCTGACCTGGATGAGCAGG--- 5900

Qy 2104 ProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSer 2123

Db 5901 -----CCGGGACTC-----CTTCGAACCCAGTCC 5924

Qy 2124 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGln 2143

Db 5925 TTTTACCACCTCACTGG-TCCAGCAACACAGTAAACGGGCACCATGTGCCACGCCGACGT 5983

Qy 2144 GluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163

Db 5984 TTGCTGCCCCCCACGCCTGCAAGTGGAAAGCCCTCCTTCCACCATCCAG-----TGT 6034

Qy 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183

Db 6035 CTGCAACGCCAGGGC-----AGTTGT 6055

Qy 2184 LeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeu----- 2199

Db 6056 GAAGATT---ACCTATCCAGGCACCTACCATCTGTGGACGGACCTCAGGACCAAGCAG 6111

Qy 2200 GlyGlyGlnProLeuGlyProGlySerArgProLysLysLeuSerProPro--- 2218

Db 6112 GGCTCAGGGTTCTGGGCAGCCCTCCTCAGAAAGGTGCACTGTATATGCCCCCTGTT 6171

Qy 2218 ----- 2218

Db 6172 GTTGTGGAGGAATCTACAGTGGGTGAAGGATACCTTGGCAAACTTGGCGGCCACTGCG 6231

Qy 2219 -----SerIleSerIleAspProProGluSerGlnGlySerArgProPro--- 2233

Db 6232 TACCTTCACCTGTCTGCAAGTGGCTGGAGCTCATCCGAATCCAGCACCCGCAAGAGGG 6291

Qy 2234 ---Cys-----SerProGlyValCysLeuArgArgAlaProAlaSerAspSerLys 2250

Db 6292 CAGTGTGACAGTTTGGTGGAGGCTGTGCTCATCTCCGAAGGCCTAGGTCTCTTTGCCCA 6351

Qy 2251 AspProSerValSerSerPro-----LeuAspSerThrAlaAlaSerProSerPro 2267

Db 6352 AGACCCAGGATTTGTGGCCCTGGCCCAAGCAGGAGATTCAGATGCATGTACCTGACCCT 6411

RESULT 2

BC051413 6035 bp mRNA linear HTC 19-NOV-2003

LOCUS Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,

DEFINITION mRNA (cDNA clone IMAGE:6493332), containing frame-shift errors.

ACCESSION BC051413

VERSION BC051413.1 GI:30802106

KEYWORDS HTC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 6035)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,I.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 6035)

Strausberg,R.

Direct Submission

Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 108 Row: 0 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

FEATURES

source

1. 6035
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:649332"
/tissue_type="Eye, retina, mouse strain C57Bl/6"
/clone_lib="NIH MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.:	3.53e-106	Length:	6035
Score:	1698.00	Matches:	615
Percent Similarity:	38.96%	Conservative:	338
Best Local Similarity:	25.14%	Mismatches:	767
Query Match:	14.12%	Indels:	730
DB:	3	Gaps:	83

US-09-611-257A-24 (1-2287) x BC051413 (1-6035)

QY 37 ArgArgMetGluArgAlaProArgSerArgAsp---SerProValAlaSerArgSerSer 55

Db 12 AGGAGGATGTCGAATCTGAAGTCGGGAAGATACAAACCCAGAGCCCAGTCAGCCCAAT 71

QY 56 ThrThr-----CysProGlyPro----- 61

Db 72 GGGACTGGCCCTGGCCCTGAATGGGGCTCTGTCTCGGCTCCAACTGTGGGGACTGAT 131

QY 62 -----GlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGlu 79

Db	132	ACCAGCGGGCGTCAGGCCTGGGACCCCAAGAAAGAGGACCCAGCACAAACACAAG	191
QY	80	AlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAsp	99
Db	192	ACTGTGGCGGTGGCCAGTGTCTCAGAGATCACCTCGAGCGCTCTTCTGCCTCACCCTTACT	251
QY	100	SerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp-----PheGluArg	117
Db	252	AATCCCATTCGTGGTCTCTGCATCAGCATTGTA-----GAGTGAAGCCTTTTGATATT	305
QY	118	ValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlu	137
Db	306	CTCATCTCTCTGACAATCTTTGCCAACTGCGTGGCATTTGGGGGTATATATCCCCCTTCCCT	365
QY	138	AspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe	157
Db	366	GAGGACGACTCCAACACTGCTAACCAACAACCTTGGAAACAGTA-----GAATACGTGTTTC	419
QY	158	--AlaPhePheAlaValGluMetValValLysMetValAlaLeuGly---IlePheGly	175
Db	420	CTGGTGATTTTACCCTGGAGACAGTGTCTCAAGATCGTAGCTATGGGTGGTGTCCAT	479
QY	176	LysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGly	195
Db	480	CCCAGCGCCTATATTCGCAATGGCTGGAACCTGCTCGACTTCATCATCGTCGTGGTGGG	539
QY	196	MetLeuGluTyrSerLeuAspLeu-----	203
Db	540	CTGTTACGCGTCTGCTGGAAACAAGGACCTGGGGCCGAGAGATGCCCCGCATACTGGA	599
QY	204	-----GlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu	220
Db	600	GGAAGCCAGGAGGCTTCGATGTAAAGGCACCTGCGGGCATTTAGGTGCTACGACCTCTA	659
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu	240
Db	660	AGGCTAGTGTCTGGGGTCCCAGTCTGCACATAGTGTCAATCCCATCATGAAGGCGCTT	719
QY	241	ProMetLeuGlyAsnValLeuLeuCysPhePheValPheIlePheGlyIleVal	260
Db	720	GTGCGCGTGTGCACATTCGCCCTGTGTGTGTCTTTCGTCAATTATCATTTACGCCATCATC	779
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
Db	780	GGACTCGAGCTATTCTCTGGACGAATGCACAAGACATGCTACTTC-----	824
QY	281	LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro	300
Db	825	-----CTGGGATCTGATATGGAA-----GCAGAGAGAGAGACCCATCACCT	863
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
Db	864	-----TGTCATCT-----	872
QY	321	ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer	340
Db	873	-----TCTGGCTCTGGCGGTTTCATGCACACTGAAC-----	902
QY	341	SerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis	360
Db	903	-----CATACCGAGTGCCCGGGCGCTGGCCA	929
QY	361	AsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePhe	380
Db	930	GGACCCCAACGGTGGCATCAGAACTTCGACAATTTTCTTTGCCATGCTAACTGTGTTC	989
QY	381	GlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSer	400
Db	990	CAGTGATATACCATGGAGGCTGGACAGACGCTCTCTACTGGATGCAGGATGCCATGGGG	1049
QY	401	Phe---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIle	419
Db	1050	TATGAGCTGCCTTGGGTGTTACTTTGTGAGCCTTGTCATCTTTGGGTCTCTTCTTGTCTC	1109

QY	1839	lnPheValLeuValAsnValValIleAlaValLeuMet-	1851
Db	4284	CTTCTCTGATTATAAATCTCTTTGTGGCTGTAATCATGGATAACTTTGATTACCTAACCA	4343
QY	1852	-----LysHisLeuGluGluSerAsnLysGluAlaLysGluG	1864
Db	4344	GAGATTGGTCTATCCTGGGACCCCACTTGTGATGATTC--AAGAGGATCTGGTCTG	4400
QY	1864	luAlaGluLeuGluAlaGluLeuGlu-----MetLysT	1877
Db	4401	AATATGACCCCGGAGCCAAGGGCCGACATCAAGCACTTGGATGTGGTTGCCCTGCTGAGAC	4460
QY	1877	hrLeuSerProGln-----ProHisSer-	1884
Db	4461	GCATCCAGCCCTTGGGATTGGAAAGCTATGCCCAACACCGAGTGGCCTGCAAGAGAC	4520
QY	1885	-----ProLeuGlySerProphe-	1891
Db	4521	TCGTGGCAATGAATGTGCCCTCAACTCAGA-TGGAACAGTGACATTCAACGCTACACTC	4579
QY	1891	euTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHist	1911
Db	4580	TTTGGCCCTGGTCGGACATCCCTGAAGATCAAGACAGAGGGAACCTGGATCAAGCCAAC	4639
QY	1911	hrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetVal----	1929
Db	4640	CAGGAGCTTCGGATGGTTCATCAAAAAGATCTGGAAGCGGATAAAGCAGAAATGTTGGAT	4699
QY	1930	--ProHisProGlu-----GluValP	1936
Db	4700	GAGGTCAATCCCTCTCCCGATGAGGAGGAGTCACTGTGGGAAAATTCTATGCCACATTC	4759
QY	1936	roValPro---LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrH	1955
Db	4760	CTGATCCAAGATTATTCCGAAAATTCGGAGAGGAAAGAAAGGGCTACTAGGAAGA	4819
QY	1955	isSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSer----	1973
Db	4820	GAGGC---CCCAACAAGCACATCTCTGCCCTCCAGGCTGGTCTTAAGGAGCCTGCAGGAC	4876
QY	1974	-----LeuGlyHisArgGlyTrpGlyL	1981
Db	4877	TTGGGTCTGAGATCCGTCAAGCCCTCACCTATGACACTGAGGAAGAAGAGAGAGGAA	4936
QY	1981	euProLysAlaGlnSerGly-----SerIleLeuS	1991
Db	4937	GAGGCAGTGGGTCAAGAGGCTGAGGAAGAGGAGTGAACAACCCAGAACCATACAAA	4996
QY	1991	erValHisSerGlnProAla-----AspThrSerCysIleLeuG	2004
Db	4997	GACTCCATAGACTCCAGCCCCAATCTCGATGGAACCTCTAGGATTT-CGGTGTCTTACC	5055
QY	2004	lnLeuProLysAspValHisTyrLeuGlnProHisGlyAlaProThrTrpGlyAlaI	2024
Db	5056	TGTTAAGGAGAACTTCCAGATTCTCTCAACTGGGCGGAGTGATGATGGGC----	5111
QY	2024	leProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnA	2044
Db	5112	-----TGGCTCCCAACTCCAGGC---AGCCAGTGTATACAGGCTGGCTCCCAACCACA	5163
QY	2044	laAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuS	2064
Db	5164	CA-----G	5166
QY	2064	erGluValSerGlyProSerCysProLeuThrArg-----SerSerSerP	2079
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QY	2079	heTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL	2099
Db	5227	AACTCAGGGCAGGACAATCAGATGAGGAACAGGAAGTCCCTGACTGGACTCTTGACCT	5286

QY	2099	ySHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp	2119
Db	5287	GGATGAGCAGG-----CCGGGACTC-----C	5307
QY	2119	roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL	2139
Db	5308	TTCGAACCCAGTCCTTTTACACCTCACTGG-TCCAGCAACACGTAAACGGGACCACATG	5366
QY	2139	euProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValG	2159
Db	5367	TGCCACGCCGACGTTTGTGTCGCCCCACGCTGCAGTCGGAAGCCCTCCTTCACCATCC	5426
QY	2159	luThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerI	2179
Db	5427	AG-----TGCTGCAACGCCAGGC-----	5446
QY	2179	leAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerL	2199
Db	5447	-----AGTTGTGAAGATT-----ACCTATCCAGGCACCTACCATCGTGACGGACC	5494
QY	2199	eu-----GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysL	2215
Db	5495	TCAGGACCAAGCAGGGTTCAGGGTTCCTGGGCAGCCCTCCTCAGAAGGGTCGACTGCTA	5554
QY	2215	euSerProPro-----	2218
Db	5555	TATGCCCCCTGTTGTTGGTGGAGGAATCTACAGTGGGTGAAGGATACCTTGGCAAACTT	5614
QY	2219	-----SerIleSerIleAspProProGluSerGlnGlySerArgP	2232
Db	5615	GGCGGCCCACTCGGTACCTTCACTGTCTGCAAGTGCCTGGAGCTCATCCGAATCCCAGC	5674
QY	2232	roPro-----Cys-----SerProGlyValCysLeuArgArgAlaProA	2246
Db	5675	CACCGCAAGAGGGCAGTGTGACAGTTTGGTGGAGGCTGTGCTCATCTCCGAAGGCCTA	5734
QY	2246	laSerAspSerLysAspProSerValSerSerPro-----LeuAspSerThrAlaA	2263
Db	5735	GGTCTCTTTGCCAAGACCACGAGATTGTGGCCCTGGCCCAAGCAGGAGATTGCAGATGCA	5794
QY	2263	laSerProSerPro 2267	
Db	5795	TGTCACCTGACCCT 5808	
RESULT 3			
BI905383			
LOCUS 603167426F1 NCI_CGAP_Lu33 Mus musculus cdna clone IMAGE:5255383 S',			
DEFINITION mRNA sequence.			
ACCESSION BI905383			
VERSION BI905383.1 GI:16167886			
KEYWORDS EST,			
SOURCE Mus musculus (house mouse)			
ORGANISM Mus musculus			
REFERENCE 1 (bases 1 to 990)			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11645 row: d column: 08 High quality sequence stop: 911.			
FEATURES			
Location/Qualifiers			

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source
1. .990
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5255383"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5,
TGTTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Alignment Scores:

Pred. No.:	3.84e-87	Length:	990
Score:	1406.00	Matches:	293
Percent Similarity:	90.77%	Conservative:	2
Best Local Similarity:	90.15%	Mismatches:	22
Query Match:	11.69%	Indels:	9
DB:	4	Gaps:	2

US-09-611-257A-24 (1-2287) x BI905383 (1-990)

QY 1823 AsnThrValIleSerProIle-TyrPheValSerPheValLeuThrAlaGlnPheValle 1842
|||||
Db 1 AACACCGTCATCTCACCCATCGTACTTCGTGTCCTCGTGCTGACGGCCAGTTTGCT 60
QY 1842 uValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLy 1862
|||||
Db 61 GGTCAACGTGGTCATAGCCGTGCTGATGAAGCACTGGAAGAGAGACAAAGAGGCCAA 120
QY 1862 sGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnPr 1882
|||||
Db 121 GGAGAGGCGGAGTTGGAGCGGAGCTGGAGCTAGAGATGAAGACACTCAGCCCGCAGCC 180
QY 1882 oHisSerProLeuGlySerPropheLeuTrpProGlyValGluGlyValAsnSerThrAs 1902
|||||
Db 181 CCACCTCCCGCTGGCGAGCCCTTCCTCTGGCCTGGGTGGAAGGTGTCAATAGCCCTGA 240
QY 1902 pSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla---SerGlyPh 1921
|||||
Db 241 CAGCCCTAAGCCTGGGGCTCCACACACCAGCCGCACATTGGAGCAGCTCTTCAGGCTT 300
QY 1921 eSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyPr 1941
|||||
Db 301 CTCCTTGAGCACCCACCGATGGTACCTCACACTGAGGAGGGGCCAGTCCCCCTAGGACC 360
QY 1941 oAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSe 1961
|||||
Db 361 AGACCTGCTGACTGTGAGGAAGTCTGGTGTACGCCGACACACTCTCTGCCCAATGACAG 420
QY 1961 rTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLe 1981
|||||
Db 421 CTACATGTGCCGAATGGGAGCACTGCCGAGAGATCCCTAGGACACAGGGGCTGGGGGCT 480
QY 1981 uProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCy 2001
|||||
Db 481 CCCCAAGCCAGTCAGGCTCCATCTGTCTGTCTCACTCCCAACCAGCAGACACCAGCTG 540
QY 2001 sIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTr 2021
|||||
Db 541 CATCCTACAGCTTCCCAAGATGCACACTATCTGCTCAGCCCTCATGGGGCTCCACCTG 600
QY 2021 pGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuAr 2041
|||||

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Db 601 GGGCGCCATCCCTAAACTACCCACCTGGCCGCTCCCTCTGGCTCAGAGGCCTCTCAG 660
QY 2041 gArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAs 2061
|||
Db 661 GCGCCAGGAGCAATAAGGACTGACTCCCTGGACGTGCAGGCGCTGGGTAGCCGGAAGA 720
QY 2061 pLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrp-G 2081
|||
Db 721 CCTGTTGTTCAGAGGTGAGTGGGGCCTCTGCCCCTCTGACCCGTCC-TCATCCTTCTGGG 779
QY 2081 lyGlySerSerIleGlnValGlnGlnArgSer---GlyIleGlnSerLysValSerLys- 2099
|||
Db 780 GCGGTTCGAGCATCCATGTGCCAGAGGCGCTCCGGCGAGCCAGAGCAAAAGTCTCCAAGG 839
QY 2100 HisIleArgLeuPro-AlaProCysPro-GlyLeuGlu-ProSerTrpAlaLysAspPro 2118
|||
Db 840 CACATCCGGCTGCCAGGCCCTTGCCAGGCGCTGGAACCCAGGCTGGGCCCAAGACCTC 899
QY 2119 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2138
|||
Db 900 AAGAGAACCCAGAAAGCAGTTAAACTTGGACCGGAGCTGAAGCTGGGATCAGGGGAACTC 959
QY 2139 Leu 2139
|||
Db 960 TTG 962
RESULT 4
BI736618
LOCUS
DEFINITION BI736618.1 GI:157113631
ACCESSION BI736618
VERSION BI736618.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11936 row: b column: 23
High quality sequence stop: 853.
FEATURES
Location/Qualifiers
1. .939
/organism="Mus musculus"
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/clone="IMAGE:5367862"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 9.39e-86 Length: 939
Score: 1385.50 Matches: 282
Percent Similarity: 92.48% Conservative: 1
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Best Local Similarity: 92.16% Mismatches: 18
Query Match: 11.52% Indels: 8
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x BI736618 (1-939)

QY	1950	GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThr	1969
Db	3	GGTGTACGCGGACACACTCTCTGCCAATGACAGCTACATGTGCCGAATGGGAGCACT	62
QY	1970	AlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIle	1989
Db	63	GCCGAGAGATCCCTAGGACACAGGGCTGGGGCTCCCCAAGCCCAGTCAGGCTCCATC	122
QY	1990	LeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspVal	2009
Db	123	TTGTCTGTTCACTCCCAACCAGCAGACACAGCTGCATCCTACAGTTTCCCAAGATGCA	182
QY	2010	HisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProPro	2029
Db	183	CACATATCTGCTCCAGCCTCATGGGGCTCCACCTGGGGCGGCATCCCTAAACTACCCCA	242
QY	2030	ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp	2049
Db	243	CCTGGCCGCTCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGAC	302
QY	2050	SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro	2069
Db	303	TCCCTGGACGTGACGGCCCTGGGTAGCCGGGAAGACCTGTGTGACAGGTGAGTGGGCC	362
QY	2070	SerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGln	2089
Db	363	TCCTGCCCTTGACCCGCTCCTCATCTTCTGGGGCGGGTCGAGCATCCAGGTGACGAG	422
QY	2090	ArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGly	2109
Db	423	CGTCCGGGACCCAGAGCAAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGCCAGGC	482
QY	2110	LeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThr	2129
Db	483	CTGGAACCCAGCTGGGCCAAGGACCTCAAGAGACCAGAGCTTAGAGCTGAGACACG	542
QY	2130	GluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPhePro	2149
Db	543	GAGCTGAGCTGGATTTCAGGAGACCTCCTGCCAGCAGTCAGGAAGAACCCCTGTCCCA	602
QY	2150	ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPhe	2169
Db	603	CGGGACTTGAAAAAATGCTACAGTGTAGAGGCCAGAGCTGCCGGCGCAGGCCTGGTCC	662
QY	2170	TrpLeuAspGluGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySerG1	2189
Db	663	TGGCTAGACGAACAGAGGAGACACTCCATCGCTTGTGCTGCTGGACAGCGGCTCCCA	722
QY	2189	nProArgLeuCysProSerProSerSerSerLeu-GlyGlyGlnProLeuGlyProGlys	2209
Db	723	GCCCCGCTATGTCCAAGCCCTCAAGCCTCGGGGGCCCAACCTCTGGGGGCCCTGGGGA	782
QY	2209	erArgProLysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnG	2229
Db	783	GCCGGCCTAAGAAAAAACTCAG-CCACCCAGTATCTCTATAGACCCCCGGAGAGCA--G	838
QY	2229	lySerArgProProCysSerProGlyValCysLeuArgArgArgAlaPro-AlaSerAsp	2248
Db	839	GACCCTCGGCCCCATGCAGTCT-GGCGTCTGCC-AGGAGAGG---CCGCGGCAAGGAC	893
QY	2249	SerLysAspPro 2252	
Db	894	TCGAAGGATCCT 905	

RESULT 5
BM479323 1076 bp mRNA linear EST 05-FEB-2002
LOCUS BM479323

DEFINITION AGENCOURT_6418725 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502230
5', mRNA sequence.
ACCESSION BM479323
VERSION BM479323.1 GI:18528365
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM12140 row: a column: 15
High quality sequence stop: 692.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5502230"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1.06e-82 Length: 1076
Score: 1343.00 Matches: 281
Percent Similarity: 87.23% Conservative: 6
Best Local Similarity: 85.41% Mismatches: 19
Query Match: 11.17% Indels: 23
DB: 4 Gaps: 4

US-09-611-257A-24 (1-2287) x BM479323 (1-1076)

QY	1458	ArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLys	1477
Db	3	AGGAACATCACCAATAAATCGGACTGTGCCAGGCCAGTTACCGTGGTCCGGCACAAG	62
QY	1478	TyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp	1497
Db	63	TACAACCTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTGTTTGGCCTCCAGGAT	122
QY	1498	GlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIle	1517
Db	123	GGTTGGTGGACATCATGTACGATGGGCTGGATGTCTGTGGCGTGACGAGCCCATC	182
QY	1518	MetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhe	1537
Db	183	ATGAACCACAAACCCCTGGATGCTGCTGTACTTTCATCTCGTTCTGCTCATTTGCGCTTC	242
QY	1538	PheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHis	1557
Db	243	TTTGTCTGGAACATGTTTGTGGGTGGTGGTGGTGGAGAACTTCCACAAGTGTCCGAGCAC	302
QY	1558	GlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLys	1577
Db	303	CAGGAGGAAGAGGAGGCCCGCGGGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	362

Db 895 ---GGCTTCGACTGGGAGGAGTATATCAACAATAAAACAACTTTACATGGTCCCTGGC 951
QY 338 -----AsnSerSerSerAsnThrThrCysValAsnTrpAsn 349
Db 952 ATGCTAGAACCCCTTGCTCTCGGGAACACAGCTCTGACGCCGGCAATGCCAGAGGGGTTTC 1011
QY 350 GlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPhe 369
Db 1012 CAG-----TGCATGAAGCAGGAAGAAATCCCACTACGGCTACACCACTTC 1059
QY 370 AspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpVal 389
Db 1060 GACACCTTCAGCTGGGCTTCCTGGCACTGTTCGGCTCATGACTCAGGACTACTGGGAG 1119
QY 390 AspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 409
Db 1120 AACTTATACCACTGACCTTACGACGGCTGGGAAACGTACATGATCTTCTTGTCTTG 1179
QY 410 LeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGln 429
Db 1180 GTGATCTTCGTGGGTTCTTCTATTGGTGAATGATCTTGGCTGTGGTGGCCATGGCT 1239
QY 430 PheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeu 449
Db 1240 TACGAAGAG----- 1248
QY 450 SerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeu 469
Db 1249 CAGAACCAAGCAACACTGGAGGAGGCAGAGCAAGAAAGGCAGAGTTCAAGGCGATGCTG 1308
QY 470 LysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAla 489
Db 1309 GAGCAGCTC-----AAGAAGCAGCAGGAGGAGCGCGAGTCAAGAAGATGCC 1353
QY 490 IleGlyValArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGlu----- 507
Db 1354 ATT-----GAAGAAGAAGGGGAAGATGGGTA 1380
QY 508 -----ProGlnProSerGly-SerCysThrArgSerHisArgArgLeuSerValHisH 525
Db 1381 GGCTCTCCGAGGAGCTCATCTGAGCTGTCTAACTCA----- 1417
QY 525 sLeuValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuAr 545
Db 1417 ----- 1417
QY 545 gValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMe 565
Db 1418 -GTTCCAAGAGCGGAAGGAGCGTCGGAACCGACGGAAGAAGAGGAAGCAGAGGAGCTC 1476
QY 565 tLeuProProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerVa 585
Db 1477 TCTGAAG-----GGGAGCAGAGGGGGACC----- 1501
QY 585 lHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
Db 1502 -----CCGAG 1506
QY 605 oArgCysProSerGluAla-----SerGly---ArgTh 615
Db 1507 AAGGTGTTTAAGTCAGAGTCGGAAGATGGCATGAGAGGAGGAGGCTTCGGGCTGCCAGAC 1566
QY 615 rValGlySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLy 635
Db 1567 AATAGGATA-GGGAGGAAATTTTCC-----ATCAT 1595
QY 635 sAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAs 655
Db 1596 GAATCAGTCGCTGCTCAGCATC-----CCAGGCTCGCCCTTCCTTTCCCGACACAA 1646
QY 655 nIlePro-----ProGlyProPhe----- 661

Db 1647 CAGCAAAAGCAGCATCTTCAGCTTTTCGGGTCCTGGACGGTTCCGGGACCCCGGTTTCGGA 1706
QY 662 -----SerSerMetHisLysLeuLeuGluThrGlnSer-ThrGlyAlaCysH 677
Db 1707 GAACGAGTTCGACAGCAGCAGCAGCAGCAGTGGAGGAAAGTGGGGCCGCGCGACTC 1766
QY 677 isSerSerCysLysIleSerSerProCysSer----- 687
Db 1767 GCTCTTCATCCCGA---TCCGGCCCCGGAGCGCCGAGCAGCTACAGCGGTACAGCGG 1823
QY 688 -----LysAlaAspSerGlyAlaCysGlyPro----- 696
Db 1824 CTACAGCCAGTCAGCCGCTCGTCGCGCATCTTCCCCAGCCTGCGGCGCAGCGTGAAACG 1883
QY 697 -----AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluS 712
Db 1884 CAACAGCACCGTGGACTGCAATGGCTGCTGCTCATCGGGCCT-GGC-----TCGC 1936
QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db 1937 ACATCGGGCGGCTCCTGCCTGAGGCAACAACACTGAGGTGAGATTAAAG----- 1983
QY 732 laGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProA 752
Db 1984 -----A 1984
QY 752 spAlaGluProSerSerValIleAlaPheTrpArgLeuIleCysAspThrPheArgLys- 771
Db 1985 AGAAAGGCCCTGGATCGCTCTAGTCTCCATGGAAACAACCTCGCCTCCTACGGACGGAAGG 2044
QY 772 --IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrL 791
Db 2045 ACAGAAATCAACAGT-----ATAATGAGCGTGTGTACAAACACAC 2083
QY 791 eu----- 791
Db 2084 TAGTGGAAGNN 2143
QY 791 ----- 791
Db 2144 NNN 2203
QY 791 ----- 791
Db 2204 NNN 2263
QY 792 --SerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleS 811
Db 2264 NNN 2323
QY 811 erAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrG 831
Db 2324 NNNNNNNNGTGTCACTGGGATCTTTCACGCGGGAATGTTCTCTGAAGCTCATAGCCATGG 2383
QY 831 lyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleS 851
Db 2384 ATCCCTACTATTACTTCCAAGAAGGCTGGAACATTTTTCACGGAATTATCGTCTCCCTCA 2443
QY 851 erValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgL 871
Db 2444 GTTAAATGGAGCTGGGCCCTGCAGACGCTGGAGGGGCTCTCAGTGTCTCGCATCTTCCGAT 2503
QY 871 euMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVal 891
Db 2504 TGCTCCGAGTCTTCAAATTGGCCCAAGTCTTGGCCACCCTGGAACATGCTGTGATCAAGATCA 2563
QY 891 euMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheI 911
Db 2564 TTGGGAACCTCGTGGCGCCCTGGGCAACCTGACCCCTGGTGTGGCCATCATTTGCTTCA 2623
QY 911 lePheSerIleLeuGlyMetHisLeuPheGly-----CysLysP 924
Db 2624 TCCTTGGCGGTGGTGGGATGACAGCTCTTTGGAAAGAGACTACAAGGAGTGGCTCTGTAGA 2683

QY 924 heAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuT 944
 Db 2684 TCAGCCAGGAG-----TGCAAGCTCCG---CGCTGGCAGATGAACGACTTCTTCC 2731
 QY 944 rpAlaIleValThrValPheGlnIleLeuThrGlnGlu-----AspTrpAsnLysValL 962
 Db 2732 ACTCCTTCTCATCGTCTTCCGAGTGTGTGGGAGTGGATCGAGACCAGTGTGTGAAC 2791
 QY 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
 Db 2792 TTATTTCTGGCCTTGCTTCTGAG----- 2814
 QY 982 hrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnA 1002
 Db 2815 -----CTCCTCAGCGCAGACAAT 2833
 QY 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
 Db 2834 CTGGCGGCCACGGACGACGACGGGAAATGAA-----CAACCTGCAGATATCG 2881
 QY 1022 lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
 Db 2882 GTGATCCGGATCAAGAAGGCGT-----GGCCTGGGCCAA----- 2916
 QY 1042 rgLysSerLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062
 Db 2917 -----AGTGAAGGTG 2926
 QY 1062 ysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerS 1082
 Db 2927 CATGCCTTCATGCAGGCACACTTCAAGCAACGGGAGGCTGATGAAGTGAAACCTTTAGAC 2986
 QY 1082 erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
 Db 2987 GAGCTGTATGAGAAGAAGGCCAACTGCATGCCCA----- 3021
 QY 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA 1122
 Db 3022 -----CCACACCG-GCGTGGACATTACAGGAACGGCGACTTCCAGAAAAATGGAAATGG 3075
 QY 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142
 Db 3076 CACCACCTAGCGGATCGGCAAAACTG----- 3101
 QY 1142 euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgA 1162
 Db 3102 -----GACGATACCAGCTCCTCAGAA----- 3122
 QY 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS 1182
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 Db 3130 CCATCGACATCAACGCTGAGGTGGAGAGAGTCCCA----- 3164
 QY 1201 rgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaA 1221
 Db 3164 ----- 3164
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 Db 3165 -----GTGGAGCAGCCTGAGGAATACTTGGATCCAGACGCTGCTTCCAGGAGGTTGTG 3219
 QY 1241 euSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgG 1261
 Db 3220 TCCAGAGGTTCAAG-----TGCTGCCAGG 3243
 QY 1261 luArg-----AspSerTrpSerAlaTyrIlePheProProGlnSerA 1275
 Db 3244 TCAACATCGAGGAAGGACTAGGCAAGTCTGG-----TGGATC----- 3281

QY 1275 rgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuV 1295
 Db 3282 --CTGCGGAAAACCTGCTTCTCTCATTTGTGGAGCACAAATTGGTTTGAGACCTTTCATCATTT 3339
 QY 1295 alIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisS 1315
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 QY 1415 hrLeuMetSerSerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaPhePheI 1435
 Db 3679 CCTTGGTGGCGCCATCCCTCCATCATGAACGTGCTGCTGGTGTCTCATCTTCTTCTGGC 3738
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Db	4954	TCTTCTCGTCACTACATCATCTCTTCTGATCGTGGTAAACATGTACATTGCCA	5013
QY	1849	alLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGlu-----GluAlaG	1866
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QY	1922	erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA	1942
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QY	1942	spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT	1962
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QY	1982	roLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI	2002
Db	5304	-----GAGTTGGACATCCTTCGCGCAGCAGATGGAGGAGCGGTTCG	5343
QY	2002	leLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpG	2022
Db	5344	TGGCGTCCAATCCTTCCAAAGTGTCTTAC-----	5372
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CF548698			
LOCUS			
DEFINITION			
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JOURNAL			
COMMENT			
FEATURES			
source			

CF548698 879 bp mRNA linear EST 22-SEP-2003
AGENCOURT_15594508 NICHD_XGC_Brn1 Xenopus laevis cDNA clone
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CF548698 GI:34885530
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Xenopus laevis (African clawed frog)
Xenopus laevis
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 879)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14738 row: j column: 24
High quality sequence stop: 646.
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QY 1464 SerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsnPheAspAsnLeu 1483
Db 63 TCCGACTGTCTTGAGGCCAGTTACCGGTGGTCCGACACAAGTACAACCTTTGACAACCTG 122
QY 1484 GlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMet 1503
Db 123 GGCCAGGCTCTGATGTCCCTGTTGTGCTGGCCTCAAGGATGGCTGGGTGACATCATG 182
QY 1504 TyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTyr 1523
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QY 1524 MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe 1543
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QY 1564 ArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 363 CGGCGCGGGAGGAGAGCGACTAAAGAGGCTGGAGAAAAGAGAGGAATCTAATGTTG 422
QY 1580 -----SerLysGluLysGlnMetAlaGluAlaGlnCysLysPro 1592
Db 423 GACGATGAATGTCTTCGGCAGCTCAGCCAGCGCTGGTGCAGAGCCCATGTCAAACCC 482
QY 1593 TyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyr 1612
Db 483 TACTACTTGACTACTCGCGCTTCGGCTCCTCGTCCACCACCTGTGTACGACCACTAC 542
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Db 543 CTGGACCTCTTCATCACTGCTGTCATCGGGCTGAATGGTCACGATGGCCATGGAACAT 602
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Db 603 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAACTACATCTTTACCGTC 662
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DEFINITION genomic survey sequence.
ACCESSION AY416499
VERSION AY416499.1 GI:39772459
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5943)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
```

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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 5943)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 21.84% Mismatches: 840
Query Match: 10.23% Indels: 664
DB: 9 Gaps: 83
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QY 80 Ala-----GluGlyLeu----- 83
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QY 97 SerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGlu 116
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IMAGE        IMAGE:30622742 5', mRNA sequence.
CF745071
CF745071.1  GI:37641411
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
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/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dt primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag is CGAAGTCGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
ORIGIN
Alignment Scores:
Pred. No.:    6.63e-73             Length:     715
Score:         1198.00           Matches:    233
Percent Similarity: 98.73%       Conservative: 1
Best Local Similarity: 98.31%    Mismatches: 3
Query Match:   9.96%            Indels:     0
DB:              7               Gaps:       0
US-09-611-257A-24 (1-2287) x CF745071 (1-715)
QY    918 HisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLys 937
Db    3 CACCTTTTGTTGCCAGTTCGCATCTCGAACGGGATGGGACACGTTGCCAGCCGGAAG 62
QY    938 AsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAsp 957
Db    63 AATTATTGACTCCCTGCCTGGGCCCATTTGTCACTGCTTTTCAGATTCTGACTCAGGAGAC 122

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/strain="C57BL/6"
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/clone="IMAGE:6419323"
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/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EW0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 9.53e-73 Length: 810
Score: 1197.00 Matches: 246
Percent Similarity: 91.51% Conservative: 2
Best Local Similarity: 90.77% Mismatches: 11
Query Match: 9.95% Indels: 15
DB: 5 Gaps: 1

US-09-611-257A-24 (1-2287) x BU709095 (1-810)

QY 1369 ValIleAspIleLeu-ValSerMetValSerAspSerGlyThrIysIleLeuGlyMetLe 1388
Db 1 GTCATCGACATCTGTGTCTCCATGGTCTCTGACAGGGGCAACCAAGATTCTCGGCATGCT 60
QY 1388 uArgValLeuArgLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnG1 1408
Db 61 GAGGGTGCTGCGCTGCTGCGGACCCCTAGCTCCACTCAGGGTCCATCAGCCGGGCCAGGG 120
QY 1408 yLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValVa 1428
Db 121 GCTGAAGCTGGTGTAGAGACTCTGATGTCTCATCCCTCAAACCCATTGGCAACATTGTGGT 180
QY 1428 lIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLy 1448
Db 181 CATCTGCTGTGCTTCTTCATCATCTTTTGAATTCTTGGGGTGCAGCTCTTCAAAGGGA 240
QY 1448 sPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaG1 1468
Db 241 GTTCTTCGTGTGTCAGGGTGAGGACACCGAGGAACATCATCAAGTCCGACTGTGCTGA 300
QY 1468 uAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMe 1488
Db 301 GGCCAGTTACCGTGGGTCCGGCACAGTACAACTTTTGACAACTTGGGCCAGGCTCTGAT 360
QY 1488 tSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAs 1508
Db 361 GTCCCTGTTTGTGCTGGCCTCCAAGGATGGTGGTTGACATCATGTATGATGGACTGGA 420
QY 1508 pAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPh 1528
Db 421 TGCTGTGGAGTGGACACGAGCCCATCATGAACCAACCACTTGGATGTGCTCTACTT 480
QY 1528 eIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValVa 1548
Db 481 CATCTCCTTCCTCATCGTGGCCCTTCTTCGTCCTGAACATGTTTGTGGCGGTGGTGGT 540
QY 1548 lGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluG1 1568
Db 541 GGAGAACTTCCATAAGTGCAGGCAGCACCAAGAGGAGGAGGAGGAGGCGCGCGGAGGA 600

QY 1568 uLysArgIleuArgLeuGluLysLysArgArg----- 1579
Db 601 GAAGCGACTAAAGAGGCTGGAGAAAAAGAGAAGGAATCTAATGTTGGACGATGTAATTGC 660
QY 1580 -----SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTy 1597
Db 661 TTCCGGCAGCTCAGCCAGCGCTGCGTCAGAACCCAGTGCANACCCCTACTCTGACTA 720
QY 1597 rSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheI1 1617
Db 721 CTCGCGCTTCCGGCTCCC-TCGTCACACCTGTGTACAGC-CACTACCTGNA-CTCTTCAT 777
QY 1617 eThrGlyValIleGlyLeuAsnValValThr 1627
Db 778 CACTGGTGTTCATCGGGCTGAATGTGTCACG 808

RESULT 13

CF584866 952 bp mRNA linear EST 24-SEP-2003
LOCUS AGENCOURT 11360281 updated NIH_MGC_137 Mus musculus cDNA clone
DEFINITION IMAGE:6431076 5', mRNA sequence.
ACCESSION CF584866
VERSION CF584866.1 GI:35198128
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRBD12 row: f column: 01
High quality sequence start: 15
High quality sequence stop: 571.

FEATURES
source

Location/Qualifiers
1..952
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6431076"
/lab_host="DH10B"
/clone_lib="NIH_MGC_137"
/note="Organ: pancreas; Vector: pSPORT1; Site_1: SalI;
Site 2: NotI; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
islets 1 M1S1-A, and Kaestner ngn3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.57e-72 Length: 952
Score: 1195.50 Matches: 250
Percent Similarity: 81.88% Conservative: 3
Best local Similarity: 80.91% Mismatches: 31
Query Match: 9.94% Indels: 25
DB: 7 Gaps: 7

US-09-611-257A-24 (1-2287) x CF584866 (1-952)		ACCESSION	AK083220
		VERSION	AK083220.1 GI:26101130
		KEYWORDS	HTC; CAP trapper.
		SOURCE	Mus musculus (house mouse)
		ORGANISM	Mus musculus
QY	1746 LeuGlyLeuLeuPheMetLeuLeuPhePheAlaAlaLeuGlyValGluLeuPhe	REFERENCE	1 Carninci, P. and Hayashizaki, Y.
Db	34 CTGGGACTTCTCTTCATGCTATTATTTTCATCTTTGCAGCTCTGGCGTGGAGCTCTTT 93	AUTHORS	2 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
QY	1766 GlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPhe	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
Db	94 GGAGACCTGGAGTGTGATGAGACACACCCCTGTGAGGGCTTGGGCGGCATGCCACCTTT 153	JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes
QY	1786 ArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsn	MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
Db	154 AGGAACCTTGGTATGGCCTTCTGACCCCTCTCCGAGTCTCCACTGGTGACAACTGGAAT 213	PUBMED	20499374
QY	1806 GlyLeMetLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrVal	REFERENCE	11042159
Db	214 GGTATTATGAAGGACACCCCTCCGGGACTGTGACGAGGAGTCCACCTGCTACAACCCGTC 273	AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
QY	1826 IleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVal	TITLE	Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Db	274 ATCTCACCCATCTACTTCGTGCTCCTTCGTGCTGACGGCCCGAGTTTGTGCTCAACGTG 333	JOURNAL	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
QY	1846 ValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAla	MEDLINE	Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Db	334 GTCATAGCCGCTGCTGATGAACACCTGGAAGAGAGCAACAAGAGGCAAGGAGGCG 393	PUBMED	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
QY	1866 GluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnProHisSerPro	REFERENCE	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Db	394 GAGTTGGAGCGGAGCTGGAGCTAGAGATGAAGACACTCAGCCCGCAGCCCACTCCCG 453	AUTHORS	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
QY	1886 LeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLys	TITLE	RIKEN integrated sequence analysis (RISA) system--384-format
Db	454 CTGGGACGCCCTTCCTCTGGCCTGGGTGGAGGTGTCAATAGCCCTGACAGCCCTAAG 513	JOURNAL	sequencing pipeline with 384 multicapillary sequencer
QY	1906 ProGlyAlaProHisThrThrAlaHisIleGlyAlaAla---SerGlyPheSerLeuGlu	MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
Db	514 CCTGGGGTCCACACACACCGGCCACATTGGAGAGCCTCTTCAGGCTTCCCTTGAG 573	PUBMED	20530913
QY	1925 HisProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeu	REFERENCE	11076861
Db	574 CACCCCAACGATGTACCTCACACTGAGGAGGGGCCAGTCCCTTAAGACAGACCTGTG 633	AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the
QY	1945 ThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCys	TITLE	FANTOM Consortium.
Db	634 ACTGTGAGGAAGTCTGGTGTACCGCGGACACACTCTCTGCCCAATGACAGTACATGTGC 693	JOURNAL	Functional annotation of a full-length mouse cDNA collection
QY	1965 ArgAsn-GlySerThrAla-GluArgSerLeuGlyHisArgGlyTrpGlyLeu---ProL	REFERENCE	Nature 409, 685-690 (2001)
Db	694 CGCAATGGGGAGCCCTGCCCGAGAGATCCCTAAGACACAAGGGGCTGGGGGCTCCCCAA 753	AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research
QY	1983 ySAlaGlnSerGly---SerIleLeuSerValHisSerGlnProAlaAspThrSerCysI	TITLE	Group Phase I & II Team.
Db	754 AAGCCAGTCAGGGCTCCAATCTTGTCTGTTCACCTCCCAACCAAGCAGACAAC--- 809	JOURNAL	Analysis of the mouse transcriptome based on functional annotation
QY	2002 leLeuGlnLeu-----ProLysAspValHisTyrLeuLeuGlnProH	REFERENCE	of 60,770 full-length cDNAs
Db	810 -----CAGCTGGCATTCTAAAGCTTCCCAAAATGCCCAA-----CTATCTGGGT 858	AUTHORS	Nature 420, 563-573 (2002)
QY	2016 isGlyAlaProThrTrpGlyAlaIlePro-----LysL 2027	TITLE	6 (bases 1 to 4675)
Db	859 TCCAGCCCTCTCTTGGGGGGCGTCCCAACCTGGGGGGGGCCCTACCCCTCTAAAC 918	JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
QY	2027 euProProGlyArgSerPro 2034	REFERENCE	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Db	919 TAACCCCCCCCACCTTGGGGCCC 941	AUTHORS	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
RESULT 14			Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
AK083220			Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
LOCUS			Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
DEFINITION			Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
			Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
			Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
			Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
			Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
			Muramatsu, M. and Hayashizaki, Y.
			Direct Submission
			Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
			Physical and Chemical Research (RIKEN), Laboratory for Genome
			Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
			RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
			Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.jp,
			URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
			Fax:81-45-503-9216)
			cDNA library was prepared and sequenced in Mouse Genome
			Encyclopedia Project of Genome Exploration Research Group in Riken
			Genomic Sciences Center and Genome Science Laboratory in RIKEN.
			Division of Experimental Animal Research in Riken contributed to
			prepare mouse tissues.
			Please visit our web site for further details.
			URL:http://genome.gsc.riken.jp/


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Db      3322 CAAGCAG----- 3328
Qy      2061 pLeuLeuSerGluValSerGlyPro-SerCysProLeuThrArgSerSerPheTrpG 2081
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Qy      2096 ysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaL 2116
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Qy      2136 lyAspLeuLeuProSerSerGlnGluProLeuPheProArgAspLeuLysLysCyst 2156
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Qy      2156 yrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArg- 2175
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Qy      2176 --ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysPros 2195
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Qy      2215 euSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProProCysS 2235
Db      3708 -----CCAAACATA----- 3716
Qy      2235 exProGlyValCysLeuArg-----ArgArgAlaProAlaSerAsps 2249
Db      3717 -----GTCTGCTTACACGTGACACGGTGTGCATCCTGACGGGTGACCTGTCTGGGACA 3768
Qy      2249 exLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysL 2269
Db      3769 AAGGACCCTGCTCCCTGGACTCACAGATTTTCTATCGCTTGGCAGACGTTACTGTCAT 3828
Qy      2269 ysAspThrLeuSerLeuSerGlyLeuSerSerAspProThr 2282
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RESULT 15
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LOCUS      771 bp      mRNA      linear      EST 26-AUG-2002
DEFINITION UI-M-FR0-cak-a-11-0-UI.r1 NIH_BMAP_FR0 Mus musculus cDNA clone
IMAGE:6413458 5', mRNA sequence.
ACCESSION BU058818
VERSION    BU058818.1 GI:22499107
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 771)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Jim Lin, University of Iowa
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
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/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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ORIGIN

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Alignment Scores:
Pred. No.:      4.03e-72      Length:      771
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Percent Similarity: 94.09%      Conservative: 1
Best Local Similarity: 93.70%      Mismatches: 15
Query Match:     9.87%      Indels:      2
DB:              5          Gaps:          0

US-09-611-257A-24 (1-2287) x BU058818 (1-771)

Qy      1580 SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1599
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Qy      1640 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal 1659
Db      190 GACGAGGCTCTGAAGATCTGCAACTACATCTTTACCGTCATCTTTGTCTTGGAGTCAGTA 249
Qy      1660 PheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgPheAsnGlnLeuAsp 1679
Db      250 TTCAAACCTTGTGGCCTTCGGCTTCGGCCGGTCTTCCAGGACAGGTGGAACCGAGCTGGAC 309
Qy      1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699
Db      310 CTGGCTATTGTGCTTCTGTCCATCATGGGCATCACGCTGGAAGAGATTGAGGTCAATGCT 369
Qy      1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719
Db      370 TCACCTGCCCATCAACCCACCATCATCCGTATCATGAGGGTGTCTCCGCAATTGCTCGAGTT 429
Qy      1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739
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Db	430	CTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGGACACGGTGATGCAGGCC	489
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Qy	1760	LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu	1779
Db	550	CTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTG	609
Qy	1780	GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer	1799
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Qy	1800	ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSer	1819
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Job time : 9822 secs